

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 16:56:17 ; Search time 69 Seconds
(without alignments)
6396.857 Million cell updates/sec

Title: US-09-784-423-32

Perfect score: 1000

Sequence: 1 GGTGTGACCTATCTCTCT.....CAGATGATGACCGCGTGC 1000

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1000	100.0	1000	3	US-09-018-584A-32
2	51	5.1	658	3	US-08-998-416-595
3	50	5.0	111282	4	US-09-754-250-3
4	47	4.7	1947	2	US-08-989-925-2
5	47	4.7	66804	4	US-09-740-041-3
6	46	4.6	17000	4	US-09-679-299A-18
7	46	4.6	90541	4	US-09-759-359A-3
8	45	4.5	43950	4	US-09-735-934A-3
9	45	4.5	43950	4	US-10-060-332-3
10	45	4.5	70000	4	US-08-851-896-3
11	44	4.4	3609	4	US-09-705-299-11
12	44	4.4	9862	4	US-09-691-861A-3
13	44	4.4	55298	4	US-09-491-356C-1
14	44	4.4	59065	4	US-09-813-817-3
15	44	4.4	59065	4	US-09-813-817-3
16	44	4.4	59065	4	US-09-978-197-3
17	44	4.4	59065	4	US-09-978-197-3
18	44	4.4	64467	4	US-09-803-671B-3
19	44	4.4	87350	3	US-08-781-891-79
20	44	4.4	87350	4	US-09-618-166-79
21	44	4.4	87543	4	US-09-791-211-3
22	43	4.3	1001	4	US-09-671-317-258
23	43	4.3	1001	4	US-09-671-317-259
24	43	4.3	1001	4	US-09-671-317-260
25	43	4.3	20598	4	US-09-593-995-10
26	43	4.3	21234	4	US-09-810-671-3
27	43	4.3	46718	4	US-09-816-093-3

C	28	4.3	74962	4	US-09-685-853A-3	Sequence 3, Appli
	29	4.3	84495	4	US-09-797-906-3	Sequence 3, Appli
C	30	4.2	2542	1	US-08-441-370-1	Sequence 1, Appli
	31	4.2	2784	1	US-08-471-454-1	Sequence 1, Appli
	32	4.2	2784	2	US-08-466-974-1	Sequence 1, Appli
	33	4.2	2784	2	US-08-471-453-1	Sequence 1, Appli
C	34	4.2	3441	4	US-09-026-033-17	Sequence 17, Appli
C	35	4.2	3451	4	US-09-811-286-1	Sequence 17, Appli
C	36	4.2	90541	4	US-09-759-359A-3	Sequence 1, Appli
C	37	4.2	162450	4	US-09-345-882-1	Sequence 3, Appli
	38	4.1	1094	4	US-09-203-256-42	Sequence 42, Appli
	39	4.1	1110	4	US-09-511-625B-43	Sequence 43, Appli
C	40	4.1	1437	6	5187077-16	Patent No. 5187077
	41	4.1	1437	6	5427925-14	Patent No. 5427925
C	42	4.1	1554	1	US-08-370-975B-10	Sequence 10, Appli
C	43	4.1	1701	3	US-09-078-294-3	Sequence 9, Appli
C	44	4.1	6330	4	US-09-880-427-2	Sequence 2, Appli
C	45	4.1	6330	4	US-09-306-538B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-018-584A-32
; Sequence 32, Application US/09018584A
; Patent No. 6238863

GENERAL INFORMATION:

APPLICANT: Schumm, James W.
APPLICANT: Bacher, Jeffery W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM REPEAT DNA MARKERS
TITLE OF INVENTION: REPEAT DNA MARKERS
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Promega Corporation
STREET: 2800 Woods Hollow Road
CITY: Madison
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: 53711-5399

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
COMPUTER: IBM compatible PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97 (DOS text format)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,584A
FILING DATE: 04-Feb-1998
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Grady J. Frenchick
REGISTRATION NUMBER: 29,018
REFERENCE/DOCKET NUMBER: 16026.9180
TELEPHONE: (608) 257-3501
TELEFAX: (608) 257-2275
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:

LENGTH: 1000 bp
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Circular
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
IMMEDIATE SOURCE:
CLONE: S132
POSITION IN GENOME: 22
CHROMOSOME/SEGMENT: 22

US-09-018-584A-32

Query Match 100.0%; Score 1000; DB 3; Length 1000;
Best Local Similarity 100.0%; Pred. No. 0;

	Matches	1000;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	GGTGTGACCTTAATCCTCTCTGAACCTCAGTTTCCTCATCGTAAATGAAAAGCTGTAG	60							
Db	1	GGTGTGACCTTAATCCTCTCTGAACCTCAGTTTCCTCATCGTAAATGAAAAGCTGTAG	60							
Qy	61	ATTGTTGTAAAAAATAATGGAAATAGGCTAGGCGCGGTGCCTCAGCGCTGTAAATCCCA	120							
Db	61	ATTGTTGTAAAAAATAATGGAAATAGGCTAGGCGCGGTGCCTCAGCGCTGTAAATCCCA	120							
Qy	121	GCATTTTAGAAGGTGCAAGAGAGGGTGGATCACITTGAGGTTCAGAGATTTTTGAGACAGCCTG	180							
Db	121	GCATTTTAGAAGGTGCAAGAGAGGGTGGATCACITTGAGGTTCAGAGATTTTTGAGACAGCCTG	180							
Qy	181	GCCACACGGTGAATCCCACCTCTCTACTAAAAATAAAAAATTAGTGGGTGCGGTGGCT	240							
Db	181	GCCACACGGTGAATCCCACCTCTCTACTAAAAATAAAAAATTAGTGGGTGCGGTGGCT	240							
Qy	241	CACACCTGTAATCCACGACACTTTGGAGGCTGAGACGGGTGGATCACCTGAGTCTCAGNG	300							
Db	241	CACA-CTGTAATCCACGACACTTTGGAGGCTGAGACGGGTGGATCACCTGAGTCTCAGNG	300							
Qy	301	TTCAAAGGCCAGCTCGGGCAACATGGTGAACACCACCTCTACTAAAAATCAAAAAATTAG	360							
Db	301	TTCAAAGGCCAGCTCGGGCAACATGGTGAACACCACCTCTACTAAAAATCAAAAAATTAG	360							
Qy	361	CCAGGTGTGGTGCCACACGCTGTAGTCCGACACTCTCTGGAGGCTGAGGCGGAGAATC	420							
Db	361	CCAGGTGTGGTGCCACACGCTGTAGTCCGACACTCTCTGGAGGCTGAGGCGGAGAATC	420							
Qy	421	GCTTGAACCCACGATAGGCAGAGTTGCAGT'GAGCCGAGATTAAGAGT'CATCTGCACCTCCAGCC	480							
Db	421	GCTTGAACCCACGATAGGCAGAGTTGCAGT'GAGCCGAGATTAAGAGT'CATCTGCACCTCCAGCC	480							
Qy	481	TGGGTGCACAGCAGACACTCCCTCTCAGAAAAATAAATAAAAAATAAAAAATAAAATAA	540							
Db	481	TGGGTGCACAGCAGACACTCCCTCTCAGAAAAATAAATAAAAAATAAAAAATAAAATAA	540							
Qy	541	AATAAATAAAAAATAAATAAATAAAGGCTGCATTTGCGCTAGCAGCTATATGCCCAATA	600							
Db	541	AATAAATAAAAAATAAATAAATAAAGGCTGCATTTGCGCTAGCAGCTATATGCCCAATA	600							
Qy	601	AGTAATAGCTATCAATATCCCCACCTCACCAGTGTGCTGAAATTAGTTTCTTTTGTGTC	660							
Db	601	AGTAATAGCTATCAATATCCCCACCTCACCAGTGTGCTGAAATTAGTTTCTTTTGTGTC	660							
Qy	661	ACCCGCCATTAGACTTTAAGGCAGAAATCTCAGCGTACTCTCTGTGTAATTTCTGTGTTCT	720							
Db	661	ACCCGCCATTAGACTTTAAGGCAGAAATCTCAGCGTACTCTCTGTGTAATTTCTGTGTTCT	720							
Qy	721	GGCACAATAGTTGGGTCTCAGTGAATAATGGT'GAGTGAAT'GAGCAAATSCAAGAAATCTCC	780							
Db	721	GGCACAATAGTTGGGTCTCAGTGAATAATGGT'GAGTGAAT'GAGCAAATSCAAGAAATCTCC	780							
Qy	781	AGGCCATCTGGAGAGCCCTCCAGCGGGGTGAGTTGGGAAATCATAGTGTGCTCTCAAT	840							
Db	781	AGGCCATCTGGAGAGCCCTCCAGCGGGGTGAGTTGGGAAATCATAGTGTGCTCTCAAT	840							
Qy	841	GGCCCACTGAAAGGTAGAGATTCTGGGTCCCACTCCGCAACCCCATCTCTCTGACTCAC	900							
Db	841	GGCCCACTGAAAGGTAGAGATTCTGGGTCCCACTCCGCAACCCCATCTCTCTGACTCAC	900							
Qy	901	TGCTGAAAAATAAATAAATAAATAAATAAACACTATTCGGAGGCTCCCAATGCGCTTGC	960							
Db	901	TGCTGAAAAATAAATAAATAAATAAATAAACACTATTCGGAGGCTCCCAATGCGCTTGC	960							
Qy	961	CAGGACTGCAAGAGCCACGACGAATGATGACCGGGGTGC	1000							
Db	961	CAGGACTGCAAGAGCCACGACGAATGATGACCGGGGTGC	1000							

[illegible]

; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 90541
; TYPE: DNA
; ORGANISM: Human
US-09-759-359A-3

Query Match 4.6%; Score 46; DB 4; Length 90541;
Best Local Similarity 100.0%; Pred. No. 6.1e-13;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 AGACACCTGGCCACACGCTGAACCCCATCTCTACTAAAAATA 215
|||||
Db 35303 AGACACCTGGCCACACGCTGAACCCCATCTCTACTAAAAATA 35258
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RESULT 8

US-09-735-934A-3
; Sequence 3, Application US/09735934A
; Patent No. 6372468
; GENERAL INFORMATION:

; APPLICANT: Li, Jiayin et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO00851
; CURRENT APPLICATION NUMBER: US/09/735,934A
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 43950
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-934A-3

Query Match 4.5%; Score 45; DB 4; Length 43950;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 367 GTGGTGCCACGCGCTGTAGTCCAGCTACTTGGAGGCTGAGGC 411
|||||
Db 7510 GTGGTGCCACGCGCTGTAGTCCAGCTACTTGGAGGCTGAGGC 7554
|||||

RESULT 9

US-10-060-332-3
; Sequence 3, Application US/10060332
; Patent No. 6528294
; GENERAL INFORMATION:

; APPLICANT: Li, Jiayin et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO00851DIV
; CURRENT APPLICATION NUMBER: US/10/060,332
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 43950
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-332-3

Query Match 4.5%; Score 45; DB 4; Length 43950;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 367 GTGGTGCCACGCGCTGTAGTCCAGCTACTTGGAGGCTGAGGC 411
|||||
Db 7510 GTGGTGCCACGCGCTGTAGTCCAGCTACTTGGAGGCTGAGGC 7554
|||||

RESULT 10

US-09-851-896-3/c
; Sequence 3, Application US/09851896
; Patent No. 6410325
; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPEND
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0220
; CURRENT APPLICATION NUMBER: US/09/851,896
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
; LENGTH: 70000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

US-09-851-896-3

Query Match 4.5%; Score 45; DB 4; Length 70000;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 512 ATAAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 556
|||||
Db 35889 ATAAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 35845
|||||

RESULT 11

US-09-705-299-11
; Sequence 11, Application US/09705299
; Patent No. 6440737
; GENERAL INFORMATION:

; APPLICANT: Lex M. Coweert
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR APOPTOSIS SUSCEPTIBILITY GENE E
; FILE REFERENCE: RTS-0174
; CURRENT APPLICATION NUMBER: US/09/705,299
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 86
; SEQ ID NO 11
; LENGTH: 3609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

US-09-705-299-11

; OTHER INFORMATION:
; NAME/KEY: unsure
; LOCATION: 92
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 869
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 1385
; OTHER INFORMATION: unknown
US-09-705-299-11

Query Match 4.4%; Score 44; DB 4; Length 3609;
Best Local Similarity 100.0%; Pred. No. 5.6e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 TGGGTGGCTCACACCTGTATCCAGCATTTCGGAGGCTGAG 274
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Db 1990 TGGGTGGCTCACACCTGTATCCAGCATTTCGGAGGCTGAG 2033
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RESULT 12

US-09-691-861A-3/c
; Sequence 3, Application US/09691861A

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; Patent No. 6482935
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000892
; CURRENT APPLICATION NUMBER: US/09/691,861A
; CURRENT FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9862
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-691-861A-3

Query Match      4.4%; Score 44; DB 4; Length 9862;
Best Local Similarity 100.0%; Pred. No. 5.7e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 368 TGGTGGCACAGCTGTAGTCCAGCTACTTGGAGGCTGAGGC 411
      |||||
Db 4344 TGGTGGCACAGCTGTAGTCCAGCTACTTGGAGGCTGAGGC 4301

RESULT 13
US-09-491-356C-1/c
; Sequence 1, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491,356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 55298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (485)..(485)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (838)..(838)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (16728)..(16728)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (22750)..(22750)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (22756)..(22756)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (28519)..(28519)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (44804)..(44804)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (45002)..(45002)
; OTHER INFORMATION: n is not determined
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; NAME/KEY: misc feature
; LOCATION: (54049)..(54049)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (54226)..(54226)
; OTHER INFORMATION: n is not determined
US-09-491-356C-1

Query Match      4.4%; Score 44; DB 4; Length 55298;
Best Local Similarity 100.0%; Pred. No. 5.7e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGCTGCTCACACCTGTAAATCCAGCAGCTTTGGAGGCT 271
      |||||
Db 23025 GGGTGGGCTGCTCACACCTGTAAATCCAGCAGCTTTGGAGGCT 22982

RESULT 14
US-09-813-817-3
; Sequence 3, Application US/09813817
; Patent No. 6340583
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001178
; CURRENT APPLICATION NUMBER: US/09/813,817
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Human
US-09-813-817-3

Query Match      4.4%; Score 44; DB 4; Length 59065;
Best Local Similarity 100.0%; Pred. No. 5.7e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGTCTCTACTAAATAACAAAAATAGCCAGGTGTGTGGGCACA 377
      |||||
Db 58882 CGTCTCTACTAAATAACAAAAATAGCCAGGTGTGTGGGCACA 58925

RESULT 15
US-09-813-817-3/c
; Sequence 3, Application US/09813817
; Patent No. 6340583
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001178
; CURRENT APPLICATION NUMBER: US/09/813,817
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Human
US-09-813-817-3

Query Match      4.4%; Score 44; DB 4; Length 59065;
Best Local Similarity 100.0%; Pred. No. 5.7e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 512 ATAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAA 555
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Db 3447 ATAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAA 3404
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Search completed: January 31, 2004, 17:27:16
Job time : 72 secs

Result No.	Score	Query		Length	PB	ID	Description
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1	1000	100.0	1000	9	US-09-784-423-32		Sequence 32, Appl
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C 3	55	5.5	677	13	US-10-027-632-134421		Sequence 134421, A
C 4	55	5.5	677	13	US-10-027-632-134421		Sequence 134421, A
C 5	55	5.5	2635	12	US-10-104-047-1607		Sequence 1607, Ap
C 6	55	5.5	43183	12	US-10-085-117-7801		Sequence 1607, Ap
7	54	5.4	439	12	US-10-242-536A-7130		Sequence 48, Appl
8	54	5.4	593	13	US-10-012-697-627		Sequence 7130, Ap
9	53	5.3	307	12	US-10-074-024-634		Sequence 627, App
C 10	53	5.3	650	13	US-10-074-024-634		Sequence 634, App
C 11	53	5.3	650	13	US-10-027-632-239196		Sequence 239196, A
C 12	52	5.2	431	13	US-10-027-632-239196		Sequence 239196, A
C 13	52	5.2	431	13	US-10-027-632-278501		Sequence 278501, A
C 14	52	5.2	432	13	US-10-027-632-278501		Sequence 278501, A
C 15	52	5.2	432	14	US-10-027-632-266549		Sequence 266549, A
C 16	52	5.2	432	14	US-10-027-632-266549		Sequence 266549, A

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SEQUENCE CHARACTERISTICS:
LENGTH: 1000 bp
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Circular
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: no
IMMEDIATE SOURCE:
CLONE: S132
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 22
SEQUENCE DESCRIPTION: SEQ ID NO: 32
US-09-784-423-32

Query Match      100.0%; Score 1000; DB 9; Length 1000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTGACCTTATCCTCTCTGAACCTCAGTTCCTCATFCGTTAAATGAAAGCTGCTAG 60
DB 1 GGTGTGACCTTATCCTCTCTGAACCTCAGTTCCTCATFCGTTAAATGAAAGCTGCTAG 60

QY 61 ATTGTCTTAAATAAATAAATGGAATAGCTAGGCGCGGTGGCTCAGCGCTCTAATCCCA 120
DB 61 ATTGTCTTAAATAAATAAATGGAATAGCTAGGCGCGGTGGCTCAGCGCTCTAATCCCA 120

QY 121 GCATTTAGAGGTGGAAGAGGGTGGATCACTTGAGGTGAGGAGTTTGGACAGAGCTG 180
DB 121 GCATTTAGAGGTGGAAGAGGGTGGATCACTTGAGGTGAGGAGTTTGGACAGAGCTG 180

QY 181 GCCAACAGGTGAAACCCATCTCTACTTAAATAAATAAATAAATAGCTGGGTGGCT 240
DB 181 GCCAACAGGTGAAACCCATCTCTACTTAAATAAATAAATAAATAGCTGGGTGGCT 240

QY 241 CACACCTGTAATCCAGCACCTTTGGGAGCTGAGACGGGTGGATCACTTGAAGTCAGGAG 300
DB 241 CACACCTGTAATCCAGCACCTTTGGGAGCTGAGACGGGTGGATCACTTGAAGTCAGGAG 300

QY 301 TTGAGCCAGCTGGGCAACATGGTGAACCAAGTCTCTACTTAAATAAATAAATAAATAG 360
DB 301 TTGAGCCAGCTGGGCAACATGGTGAACCAAGTCTCTACTTAAATAAATAAATAAATAG 360

QY 361 CCAGTGTGTGGCACAGCCTGTAGTCCAGCTACTTGGGAGGTGAGGCGGAGGATC 420
DB 361 CCAGTGTGTGGCACAGCCTGTAGTCCAGCTACTTGGGAGGTGAGGCGGAGGATC 420

QY 421 GCTTGAACCCAGTAGGCGAGAGGTTGAGTGAGCCGAGATAAGAGTCACTGCCAGCC 480
DB 421 GCTTGAACCCAGTAGGCGAGAGGTTGAGTGAGCCGAGATAAGAGTCACTGCCAGCC 480

QY 481 TGGGTGACAGACAGACTCCCTCTCAGAAATAAATAAATAAATAAATAAATAAATAA 540
DB 481 TGGGTGACAGACAGACTCCCTCTCAGAAATAAATAAATAAATAAATAAATAAATAA 540

QY 541 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 600
DB 541 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 600

QY 601 AGTAATAGTATCAATATCCCAACCCCTACACCTGTGCTGAAATTAGTTCTTTTGTG 660
DB 601 AGTAATAGTATCAATATCCCAACCCCTACACCTGTGCTGAAATTAGTTCTTTTGTG 660

QY 661 ACCCCCATAGACTTAAGGAGAAATTCACCGTACTCTCTGTAATTTCTGGTCTCT 720
DB 661 ACCCCCATAGACTTAAGGAGAAATTCACCGTACTCTCTGTAATTTCTGGTCTCT 720

QY 721 GGCACATAGTGGGTCTCAGTGAACATGTTGAGTGAATGAGCAATCAAGAAATCTCC 780
DB 721 GGCACATAGTGGGTCTCAGTGAACATGTTGAGTGAATGAGCAATCAAGAAATCTCC 780

QY 781 AGGCCATCTGGAGCCCTCCAGCGGGTGAATTCGGGAAATCTCATAGTCTGCTCAAT 840
DB 781 AGGCCATCTGGAGCCCTCCAGCGGGTGAATTCGGGAAATCTCATAGTCTGCTCAAT 840
```

```
QY 841 GGCCTACTGAAAGCTAGAGAGTTCTGGGTCCACCTCCGACACCCCACTCTCTGACTAC 900
DB 841 GGCCTACTGAAAGCTAGAGAGTTCTGGGTCCACCTCCGACACCCCACTCTCTGACTAC 900

QY 901 TGCTGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960
DB 901 TGCTGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960

QY 961 CAGGACTGCAAGAGAGCCCGAGCAGAGATGATGACCGGCGTGC 1000
DB 961 CAGGACTGCAAGAGAGCCCGAGCAGAGATGATGACCGGCGTGC 1000
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RESULT 2

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US-09-764-891-10051/c
; Sequence 10051, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10051
; LENGTH: 11627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-10051
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Query Match      5.8%; Score 58; DB 11; Length 11627;
Best Local Similarity 100.0%; Pred. No. 6.7e-19;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 340 TACTAAAAATACAAAAATAGCCAGGTGTGGTGGCACACGCTGTAGTCCAGTACT 397
DB 10819 TACTAAAAATACAAAAATAGCCAGGTGTGGTGGCACACGCTGTAGTCCAGTACT 10762
```

RESULT 3

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US-10-027-632-134421/c
; Sequence 134421, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134421
; LENGTH: 677
; TYPE: DNA
; ORGANISM: Human
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US-10-027-632-134421

Query Match 5.5%; Score 55; DB 13; Length 677;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 343 TAAATAACAAAATTAGCCAGGTGTGGTGGCACACGCTGTAGTCCAGCTACT 397
Db 341 TAAATAACAAAATTAGCCAGGTGTGGTGGCACACGCTGTAGTCCAGCTACT 287

RESULT 4
US-10-027-632-134421/c
; Sequence 134421, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134421
; LENGTH: 677
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-134421

Query Match 5.5%; Score 55; DB 14; Length 677;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 343 TAAATAACAAAATTAGCCAGGTGTGGTGGCACACGCTGTAGTCCAGCTACT 397
Db 341 TAAATAACAAAATTAGCCAGGTGTGGTGGCACACGCTGTAGTCCAGCTACT 287

RESULT 5
US-10-104-047-1607/c
; Sequence 1607, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cdna
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1607
; LENGTH: 2635
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1607

Query Match 5.5%; Score 55; DB 12; Length 2635;

Best Local Similarity 100.0%; Pred. No. 2.1e-17;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 318 CAACATGGTGAACACCGCTCTCTACTTAAATAATACAAAAATAGCCAGGTGTGGTG 372
Db 2019 CAACATGGTGAACACCGCTCTCTACTTAAATAATACAAAAATAGCCAGGTGTGGTG 1965

RESULT 6
US-10-085-117-28
; Sequence 28, Application US/10085117
; Publication No. US2003023234A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 43183
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-117-28

Query Match 5.5%; Score 55; DB 12; Length 43183;
Best Local Similarity 100.0%; Pred. No. 2.4e-17;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 318 CAACATGGTGAACACCGCTCTCTACTTAAATAATACAAAAATAGCCAGGTGTGGTG 372
Db 30963 CAACATGGTGAACACCGCTCTCTACTTAAATAATACAAAAATAGCCAGGTGTGGTG 31017

RESULT 7
US-10-242-535A-7130
; Sequence 7130, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C. C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 7130
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-7130

Query Match 5.4%; Score 54; DB 12; Length 439;
Best Local Similarity 100.0%; Pred. No. 6.3e-17;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 228 GGGTGGCGGTGCCTCACACCTGTATATCCAGCCTTTGGAGGCTGAGAGCGGTG 281
Db 219 GGGTGGCGGTGCCTCACACCTGTATATCCAGCCTTTGGAGGCTGAGAGCGGTG 272

RESULT 8

US-10-012-697-627
; Sequence 627, Application US/10012697
; Publication No. US20030215803A1
; GENERAL INFORMATION:
; APPLICANT: Escobedo, Jaime
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Kassam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Scott, Beth
; APPLICANT: Dmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Dmanac, Srejana
; APPLICANT: Labat, Ivan
; APPLICANT: Leishkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
; FILE REFERENCE: 2300-16252
; CURRENT APPLICATION NUMBER: US/10/012,697
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/254,648
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/275,668
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 1568
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 627
; LENGTH: 593
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 394, 404, 409, 411, 426, 432, 477, 499, 508, 525, 527, 539,
; LOCATION: 549, 555, 567, 592
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 394, 404, 409, 411, 426, 432, 477, 499, 508, 525, 527, 539,
; LOCATION: 549, 555, 567, 592
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 394, 404, 409, 411, 426, 432, 477, 499, 508, 525, 527, 539,
; LOCATION: 549, 555, 567, 592
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 394, 404, 409, 411, 426, 432, 477, 499, 508, 525, 527, 539,
; LOCATION: 549, 555, 567, 592
; OTHER INFORMATION: n = A,T,C or G
US-10-012-697-627

Query Match 5.4%; Score 54; DB 13; Length 593;
Best Local Similarity 100.0%; Pred. No. 6.4e-17;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGTGGGGTGGCTCACACCTGTAATCCAGCATTGGAGGCTTGAGACGGGTG 281

DB 94 GGTGGGGTGGCTCACACCTGTAATCCAGCATTGGAGGCTTGAGACGGGTG 147

RESULT 9

US-10-074-024-634
; Sequence 634, Application US/10074024
; Publication No. US20030232975A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC001C1
; CURRENT APPLICATION NUMBER: US/10/074,024
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 879
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 634
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-074-024-634

Query Match 5.3%; Score 53; DB 12; Length 307;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 GGTGGCTCACACCTGTAATCCAGCATTGGAGGCTTGAGACGGGTGATCA 286

DB 14 GGTGGCTCACACCTGTAATCCAGCATTGGAGGCTTGAGACGGGTGATCA 66

RESULT 10

US-10-027-632-239196/c
; Sequence 239196, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 239196
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(650)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-239196

Query Match 5.3%; Score 53; DB 13; Length 650;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 CAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 558

DB 254 CAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 202

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RESULT 11
US-10-027-632-239196/c
; Sequence 239196, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 239196
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(650)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-239196

Query Match      5.3%; Score 53; DB 14; Length 650;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 CAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 558
Db 254 CAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 202

RESULT 12
US-10-027-632-278501/c
; Sequence 278501, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 278501
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(431)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-278501

Query Match      5.3%; Score 53; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 CAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 558
Db 254 CAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 202
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RESULT 13
US-10-027-632-278501/c
; Sequence 278501, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 278501
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(431)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-278501

Query Match      5.2%; Score 52; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 TCTCTACTAAAAATACAAAAATAGCCAGGTGTGGTGGCACACGCGCTGTAGT 387
Db 376 TCTCTACTAAAAATACAAAAATAGCCAGGTGTGGTGGCACACGCGCTGTAGT 325

RESULT 14
US-10-027-632-266549/c
; Sequence 266549, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
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; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 266549
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-266549

Query Match 5.2%; Score 52; DB 13; Length 432;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 336 TCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGGCACACGCCCTGTAGT 387
Db 376 TCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGGCACACGCCCTGTAGT 325

RESULT 15

US-10-027-632-266549/c
; Sequence 266549, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 266549
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-266549

Query Match 5.2%; Score 52; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 336 TCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGGCACACGCCCTGTAGT 387
Db 376 TCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGGCACACGCCCTGTAGT 325

Search completed: January 31, 2004, 17:33:22
Job time : 356 secs

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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 15:28:31 ; Search time 90 Seconds
(without alignments)
4904.257 Million cell updates/sec

Title: US-09-784-423-32
Perfect score: 1000
Sequence: 1 GGTGTCCTTATCCCTCTCT.....CAGATGATGACCGGCGTGC 1000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	999	99.9	1000	3	US-09-018-584A-32
2	296	29.6	15297	4	US-09-817-180-3
3	284	28.4	2713	2	US-08-915-901-6
4	284	28.4	2713	4	US-09-154-602-6
5	284	28.4	7720	3	US-09-318-448-5
6	279.6	28.0	53332	4	US-09-801-861-3
7	277.8	27.8	7210	2	US-08-257-963B-10
8	277.8	27.8	7210	4	US-08-367-841A-10
9	277.8	27.8	7210	5	PCT-US95-07201-10
10	277.8	27.8	14581	4	US-08-520-373D-4
11	277.8	27.8	22481	4	US-08-367-841A-43
12	277.8	27.8	22481	5	PCT-US95-07201-43
13	277.8	27.8	22484	4	US-09-875-223-2
14	275.6	27.6	112132	4	US-09-741-150-3
15	272.6	27.3	29629	4	US-09-729-995-3
16	271.4	27.1	62804	4	US-09-800-960-3
17	269.6	27.0	59065	4	US-09-813-817-3
18	269.6	27.0	59065	4	US-09-813-817-3
19	268	26.8	66804	4	US-09-740-041-3
20	267.4	26.7	14581	4	US-08-520-373D-4
21	266.6	26.7	17327	1	US-07-906-871-15
22	265.8	26.6	7210	2	US-08-257-963B-10
23	265.8	26.6	7210	4	US-08-367-841A-10
24	265.8	26.6	7210	5	PCT-US95-07201-10
25	265.8	26.6	22481	4	US-08-367-841A-43
26	265.8	26.6	22481	5	PCT-US95-07201-43
27	265.8	26.6	22484	4	US-09-875-223-2

Sequence 3, Appli
Sequence 17, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 5, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 258, App
Sequence 259, App
Sequence 260, App
Sequence 1, Appli
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-018-584A-32
; Sequence 32, Application US/09018584A
; Patent No. 6238863
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA: US/09/018,584A
; APPLICATION NUMBER: 04-Feb-1998
; FILING DATE: 04-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Circular
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: no
; IMMEDIATE SOURCE:
; CLONE: SL32
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 22
; US-09-018-584A-32

Query Match 99.9%; Score 999; DB 3; Length 1000;
Best Local Similarity 100.0%; Pred. No. 3.7e-217;

Matches 1000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGTGACCTTATCTCTCTGAACTCAGTTCCTTCATCCGTAATAAAGAAAGCTGTAG 60
Db 1 GGTGTGACCTTATCTCTCTGAACTCAGTTCCTTCATCCGTAATAAAGAAAGCTGTAG 60

Qy 61 ATTCTTTGTAATAAATAAATTAATGTAATAGCTAGGCGGGTGGCTCAAGCTGTATCCCA 120
Db 61 ATTCTTTGTAATAAATAAATTAATGTAATAGCTAGGCGGGTGGCTCAAGCTGTATCCCA 120

Qy 121 GCATTTAGAGGTGGAAGAGGTGGATCACTTGAAGTTCAGAGGTTTTCAGACAGAGCTG 180
Db 121 GCATTTAGAGGTGGAAGAGGTGGATCACTTGAAGTTCAGAGGTTTTCAGACAGAGCTG 180

Qy 181 GCCAACACGGTGAAACCCCATCTCTACTATAAATAAATAAATAAATAAATAAATAAATA 240
Db 181 GCCAACACGGTGAAACCCCATCTCTACTATAAATAAATAAATAAATAAATAAATAAATA 240

Qy 241 CACACCTGTAATCCAGCAGCTTTGGAGAGCTGAGACGGTGGATCACTGAAGTCAGAG 300
Db 241 CACACCTGTAATCCAGCAGCTTTGGAGAGCTGAGACGGTGGATCACTGAAGTCAGAG 300

Qy 301 TTCAAGGCCAGGCTGGGCAACATGTTGAACCCAGCTCTCTACTATAAATAAATAAATAAATA 360
Db 301 TTCAAGGCCAGGCTGGGCAACATGTTGAACCCAGCTCTCTACTATAAATAAATAAATAAATA 360

Qy 361 CCAGGTGTGGTGACACAGCTGTAGTCCAGCTACTTTGGAGGCTGAGGCGGGAAGATC 420
Db 361 CCAGGTGTGGTGACACAGCTGTAGTCCAGCTACTTTGGAGGCTGAGGCGGGAAGATC 420

Qy 421 GCTTTGAACCCAGTAGGACAGAGTTGAGTGAGCCGAGATGAAGTCACTGACCTCCAGCC 480
Db 421 GCTTTGAACCCAGTAGGACAGAGTTGAGTGAGCCGAGATGAAGTCACTGACCTCCAGCC 480

Qy 481 TGGTGACAGACAGAGACTCCCTCTCAGAAAAATAAATAAATAAATAAATAAATAAATAA 540
Db 481 TGGTGACAGACAGAGACTCCCTCTCAGAAAAATAAATAAATAAATAAATAAATAAATAA 540

Qy 541 AATAAATAAATAAATAAATAAATAAAGGCTGGCACTTTGCTAGCACTTATATGCCCAATA 600
Db 541 AATAAATAAATAAATAAATAAATAAAGGCTGGCACTTTGCTAGCACTTATATGCCCAATA 600

Qy 601 AGTAATAGCTATCAATATCCACCCCTTACCACTGTCTGAAATTTAGTTTCTTTTGTG 660
Db 601 AGTAATAGCTATCAATATCCACCCCTTACCACTGTCTGAAATTTAGTTTCTTTTGTG 660

Qy 661 ACCCCCATTTAGACTTAAGGAGAAATTTCTACCCGTAATTTCTCTGTAATTTCTGTTTCT 720
Db 661 ACCCCCATTTAGACTTAAGGAGAAATTTCTACCCGTAATTTCTCTGTAATTTCTGTTTCT 720

Qy 721 GGCACATAGTTGGGTCTCAGTGAACATGGTGAATGAGCAAAATGCAAGGAATCTCC 780
Db 721 GGCACATAGTTGGGTCTCAGTGAACATGGTGAATGAGCAAAATGCAAGGAATCTCC 780

Qy 781 AGGCCATCTGGAGAGCTCCAGCGGGTGAATTCGGGAACTCATAGCTGTCTCTCAAT 840
Db 781 AGGCCATCTGGAGAGCTCCAGCGGGTGAATTCGGGAACTCATAGCTGTCTCTCAAT 840

Qy 841 GGCCCACTGAAGAGGTAGAGAGTTCTGGGTCCCACTCCGACCCCACTCTCTGACTCAC 900
Db 841 GGCCCACTGAAGAGGTAGAGAGTTCTGGGTCCCACTCCGACCCCACTCTCTGACTCAC 900

Qy 901 TGTGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960
Db 901 TGTGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960

Qy 961 CAGGACTGCAAGGAGCCCGACAGATGATGACCGGGTGC 1000
Db 961 CAGGACTGCAAGGAGCCCGACAGATGATGACCGGGTGC 1000

RESULT 2

US-09-817-180-3

; Sequence 3, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; FILE REFERENCE: CL001183
; CURRENT APPLICATION NUMBER: US/09/817,180
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Human
; US-09-817-180-3

Query Match 29.6%; Score 296; DB 4; Length 15297;
Best Local Similarity 83.4%; Pred. No. 4.6e-58;
Matches 371; Conservative 0; Mismatches 71; Indels 3; Gaps 3;

Qy 97 CGGTGGCTCAGCGCTGTATCCAGACCTTTTGAAGGTGCAAGAGGTGATCACTTGA 156
Db 11700 CAGTTGTCTACGCTGTATCCAGACCTTTTGGAGGCTGAGCTGGGTGATCACTTGA 11759

Qy 157 GTCAAGAGTTTTCAGACAGAGCTGGCCACACAGCTGGAACCCCATCTCTACTATAAATAA 216
Db 11760 CCCAGGAG-TTCAAGATCAGTTGGACACACAGTGAATCTCCATCTGTACAAAAATATC 11818

Qy 217 AAAATTAGTNGGGTGGCTGCACACCTGTATCCAGCACTTTTGGAGGCTGAGAC 276
Db 11819 AAAAATAGACTGGGACGCTGGCTACACCTGTATCCAGCACTTTTGGAGGCTGAGAC 11878

Qy 277 GGGTGGATCACTTGAAGTTCAGAGTTCAGGCGCCAGCTGGGCAACATGTGAAACAGGT 336
Db 11879 AGGTGGATCACTTGTGGTTCAGAGTTTGAAGCCAGCCAGCAACATGTGAAACAGGT 11938

Qy 337 CTCTACTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 396
Db 11939 CTCTACTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 11998

Qy 397 TTGGAGGCTGAGGCGGGAAGATGCTTGAACCCAGTAGGAGGCTGAGGCTGAGGCGGA 456
Db 11999 TTGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCGGA 12058

Qy 457 GATTAAGTCACTTGCACCTCCAGCTGGGTGAC-AGAGCAAGACTCCCTCTCAGAAATAA 515
Db 12059 GAT-TGTGCCACTGCACTCCAGCTGGGCAAGAGTGAATCTCCATCTCAAAAAAAC 12117

Qy 516 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 540
Db 12118 CAAAAACAAAAATACAAAAATA 12142

RESULT 3

US-08-916-901-6
; Sequence 6, Application US/08916901
; Patent No. 5892012
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: RAB PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,901
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-916-901-6

Query Match 28.4%; Score 284; DB 2; Length 2713;
Best Local Similarity 81.3%; Pred. No. 1.7e-55;
Matches 365; Conservative 0; Mismatches 81; Indels 3; Gaps 3;

QY 74 AATTAATGGAATAGGCTAGGCGGGTGGCTACGCGCTGTAATCCAGACACTTTAGAGG 133
Db AAAAAATCAAAATTTAGCGCGCGCTGGTGGCTCACCTGTAATCCAGACTTCTGGGAGG 1747
QY 134 TCGAAGAGGGTGGATCACTTGAGGTTCAGGAGTTTTCAGACACAGCTGGCCACACGGTGA 193
Db 1748 CTGAGGCGAGGAGTAATCACTTGAGGTTCAGGAG-TTTGAGACACAGCTGGCCACACGGTGA 1806
QY 194 AACCCCATCTCTACTAAAAATAAAAAATTAAGTNGGGTGGCGGTGCTCACCTGTAATC 253
Db 1807 AACCTGTCTCTACTAAAAATAAAAAATAAGGAGGCTAGCCAGGCGGGTGGCGGCTGTAATC 1866
QY 254 CCAGCACTTTGGGAGGCTGAGACGGGTGGATCACTTGAGGTTCAGGAGTTTTCAGACACAGCTGGCCACACGGTGA 313
Db 1867 TCAGCACTTTGGGAGGCGGAGGAGTGGATCACTTGAGGTTCAGGAGTTTTCAGACACAGCTGGCCACACGGTGA 1926
QY 314 TGGGCAACATGGTGAACACACCTCTCTACTAAAAATAAAAAATTAAGCAGGTGGTGG 373
Db 1927 TGGCCAAACATGGTGAACACACCTCTCTACTAAAAATAAAAAATTAAGCAGGTGGTGG 1986
QY 374 CACACGCTCTAGTCCAGCTACTTTGGAGGCTGAGGCGGAGAGTTCGCTTGAACCCAGT 433
Db 1987 TGCATGCTCTGTAATCCAGCTACTTTGGAGGCTGAGGCGGAGAGTTCGCTTGAACCCAGT 2046
QY 434 AGGCAGAGGTTCAGTTCAGGCGGAGATTAAGAGTCACTGCACTCCAGCTGGGTGACAGG 493
Db 2047 A-GCAGAGGTTCAGTTCAGGCGGAGATCA-TGCCACTGCACTCCAGCTGGGTGACAGG 2104
QY 494 AAGACTCCCTCTCAGAAAAATAAAAA 522
Db 2105 GAGACTCCATTTCAAAAAAAGAACTACA 2133

RESULT 4

US-09-154-602-6
Sequence 6, Application US/09154602
Patent No. 6300472
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,602
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,901
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-154-602-6

Query Match 28.4%; Score 284; DB 4; Length 2713;
Best Local Similarity 81.3%; Pred. No. 1.7e-55;
Matches 365; Conservative 0; Mismatches 81; Indels 3; Gaps 3;

QY 74 AATTAATGGAATAGGCTAGGCGGGTGGCTACGCGCTGTAATCCAGACACTTTAGAGG 133
Db AAAAAATCAAAATTTAGCGCGCGCTGGTGGCTCACCTGTAATCCAGACTTCTGGGAGG 1747
QY 134 TCGAAGAGGGTGGATCACTTGAGGTTCAGGAGTTTTCAGACACAGCTGGCCACACGGTGA 193
Db 1748 CTGAGGCGAGGAGTAATCACTTGAGGTTCAGGAG-TTTGAGACACAGCTGGCCACACGGTGA 1806
QY 194 AACCCCATCTCTACTAAAAATAAAAAATTAAGTNGGGTGGCGGTGCTCACCTGTAATC 253
Db 1807 AACCTGTCTCTACTAAAAATAAAAAATAAGGAGGCTAGCCAGGCGGGTGGCGGCTGTAATC 1866
QY 254 CCAGCACTTTGGGAGGCTGAGACGGGTGGATCACTTGAGGTTCAGGAGTTTTCAGACACAGCTGGCCACACGGTGA 313
Db 1867 TCAGCACTTTGGGAGGCGGAGGAGTGGATCACTTGAGGTTCAGGAGTTTTCAGACACAGCTGGCCACACGGTGA 1926
QY 314 TGGGCAACATGGTGAACACACCTCTCTACTAAAAATAAAAAATTAAGCAGGTGGTGG 373
Db 1927 TGGCCAAACATGGTGAACACACCTCTCTACTAAAAATAAAAAATTAAGCAGGTGGTGG 1986
QY 374 CACACGCTCTAGTCCAGCTACTTTGGAGGCTGAGGCGGAGAGTTCGCTTGAACCCAGT 433
Db 1987 TGCATGCTCTGTAATCCAGCTACTTTGGAGGCTGAGGCGGAGAGTTCGCTTGAACCCAGT 2046
QY 434 AGGCAGAGGTTCAGTTCAGGCGGAGATTAAGAGTCACTGCACTCCAGCTGGGTGACAGG 493
Db 2047 A-GCAGAGGTTCAGTTCAGGCGGAGATCA-TGCCACTGCACTCCAGCTGGGTGACAGG 2104
QY 494 AAGACTCCCTCTCAGAAAAATAAAAA 522
Db 2105 GAGACTCCATTTCAAAAAAAGAACTACA 2133

RESULT 5

US-09-318-448-5/c

Sequence 5, Application US/09318448
Patent No. 6210950
GENERAL INFORMATION:
APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 7720
TYPE: DNA
ORGANISM: Homo sapiens
US-09-318-448-5

Query Match 28.4%; Score 284; DB 3; Length 7720;
Best Local Similarity 84.9%; Pred. No. 2.1e-55;
Matches 376; Conservative 0; Mismatches 61; Indels 6; Gaps 5;

QY 87 AGCTAGGCGGGTGGCTCAAGCTGTAATCCAGCACCTTTAGAGGTTCGAGAGGGTGG 146
Db 6233 AGCTGGGTGCAGTGGCTTACTTGTGTAATCCAGCACCTTTGGAGGCCAAGCGAGGTGG 6174

QY 147 ATCACTTGAGTCAAGAGTTTGGAGCCAGCTGGCCACACAGCTGAAACCCCATCTCTA 206
Db 6173 ATCACTTGAGATCAAGAG-TTTGAGACCAGCTGGCCACACATGTTGAAACCCCATCTCTA 6115

QY 207 CTAATAAATA-TAAAAATTAGCTGGGTGGTGGCTCACACCTGTGTAATCCAGCACCTTTGG 265
Db 6114 CTAATAAATA-TAAAAATTAGCTGGGTGGTGGTGGCTCACACCTGTGTAATCCAGCACCTTTGG 6055

QY 266 GAGGCTGAGACGGGTGATCACTGAGCTCAGGAGTTCAAGGCCAGCTGGCGCAACATGG 325
Db 6054 GAGGCGAGGCGGGTGCATCAC--GAGCTTAGAGATCAAGNCCATCTCTGGCCACATGG 5997

QY 326 TGAACACACGCTCTACTAAAAATAC-AAAAAATTAGCCAGGTGGTGGCACACGCTGT 384
Db 5996 TGAACACCGCTCTCTACTAAAAATACAAAAAATTAGCCGGGCGTGGTGGCACCTGT 5937

QY 385 AGTCCACGCTACTTGGGAGGCTGAGCGGAGATCGCTGTAACCCAGTAGGAGGTT 444
Db 5936 AGTCCACGCTACTTGGGAGGCTGAGCGGAGGATGGTGAACCCGCGAGGTGGAGCTT 5877

QY 445 GCAGTGAGCCGAGATAGAGTCACTGCACTCCAGCTGGGTGACAGAGCAAGACTCCCTC 504
Db 5876 GCAGTGAGCCGAGATCA-TGCCACTGCACTCCAGCTGGGGGACAGAGCAAGACTCCATC 5818

QY 505 TCAGAAAAATAAATAAATAAAA 527
Db 5817 TCAGAAAAATAAATAAATAAAA 5795

RESULT 6
US-09-801-861-3/c
Sequence 3, Application US/09801861
Patent No. 6492154
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001098
CURRENT APPLICATION NUMBER: US/09/801,861
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 5332
TYPE: DNA
ORGANISM: Human

US-09-801-861-3

Query Match 28.0%; Score 279.6; DB 4; Length 5332;
Best Local Similarity 78.2%; Pred. No. 3e-54;
Matches 373; Conservative 0; Mismatches 100; Indels 4; Gaps 3;

QY 88 GGCTAGGCGGGTGGCTCAGCGCTGTAATCCAGCACCTTTAGAGGTTCGAGAGGGTGGGA 147
Db 25692 GGCCAGCGCGAGGACTCACATGTGTAATCCAGAACCTTTGAGAGGCCAAGCGCAGAGGA 25633

QY 148 TCACCTTGAGGTCAAGAGTTTGGAGACCAAGCTGGCCAAACACGCTGAAACCCCATCTCTAC 207
Db 25632 TTGCTTGAGTCCAGGAG-TTCGAGACCAGCTGGGCHACATAGCAAGACCCCACTCTCTAT 25574

QY 208 TAAAAATAAATAAATTAGCTGGGTGGTGGCTCACACCTGTGTAATCCAGCACCTTTGGGA 267
Db 25573 AAAAAACAAAAA--TAGGCCAGGCACAGTGGCTCATACCTGTGTAATCCAGCACCTTTGGAA 25516

QY 268 GGCTGAGACGGGTGGATCACTGAGTCAAGGAGTTCAAGGCCAGCTGGCCAAACATGGTG 327
Db 25515 GGCCAGCGCAGGTGAATCACTCAGGTCAAGGTTCAGACACAGCTGGCCACATGGTG 25456

QY 328 AAACACAGTCTCTACTAAAAATAAATAAATTAGCAGGTGGTGGTGGCACACGCTGTAGT 387
Db 25455 AAACCCCGTCTCTACTAAAAATAAATAAATTAGTCAAGTGGTGGGTGGCTGTAGT 25396

QY 388 CCCAGCTACTTGGGAGGCTGAGCGGAGAAATCGCTTGAACCCAGTAGCGAGAGTTGCA 447
Db 25395 CCCAGCTACTTGGAGAGGCTGAGCGAGGAGGCTCCCTTTGAACCCAGGAAAGCGAGTTGCA 25336

QY 448 GTGAGCCGAGATAAGAGTCACTGCACTCCAGCTGGGTGACAGAGCAAGACTCCCTCTCA 507
Db 25335 GTGAGCTGAG-TTGGCCCACTGCACTCCAGCTGGCAGCAGAGCGGAGACTCCCGCTCA 25277

QY 508 GAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 564
Db 25276 AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 25220

RESULT 7
US-08-257-963B-10
Sequence 10, Application US/08257963B
Patent No. 5840686
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, S.
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL
TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,963B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH

REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7210 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE: Human
IMMEDIATE SOURCE:
LIBRARY: DASH II
FEATURE:
NAME/KEY: JT106
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: 7.2 kb No. 5840686 1 fragments
OTHER INFORMATION: Derived from human placental genomic DNA
US-08-257-963B-10

Query Match 27.8%; Score 277.8; DB 2; Length 7210;
Best Local Similarity 82.3%; Pred. No. 5.2e-54;
Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;

QY 88 GCCTAGGCGGGTGGCTCAGCGCTGTATATCCAGCACCTTTAGAAAGTGAAGAGGGTGA 147
Db 3756 GCGCGGGCAGCGTGGCTCAGCGCTGTATCCAGCACCTTTGGAGGCCGAGGCGAGA 3815

QY 148 TCACCTTGAAGTCAGGAGTTTTCAGACCGAGCTGGCCACACGCTGTAATCCAGCACCTTTAGAAAGTGAAGAGGGTGA 207
Db 3816 TCACCTTGAAGTCAGGAG-TTCGAGACCGAGCTGGCTTAACACGATGAACCCCGTCTCTAC 3874

QY 208 TAAAAATA-AAAAATTAGCTNGGCGGTGGCTCACACCTGTATATCCAGCACCTTTGGG 266
Db 3875 TAAAAATACAAAAAATTAGCTGGGCGCGGTGGCTGTGCTGTGTATATCCAGCACCTTTGGG 3934

QY 267 AGGCTGAGAGCGGTGGATCCTTGAAGTCAGGAGTTCAAGGCCAGCGCTGGGCAACATGGT 326
Db 3935 AGGCAGAGGTGGGCGAGATCACTTGAAGTCAGGAGTTTGAAGCACGCTAGCCATGGT 3994

QY 327 GAAACCCATCTCTACTAAATAACAAAAATTAGCCAGCTTTAGAGAGTGGTGGCACGCTGTAG 386
Db 3995 GAAACCCATCTCTACTAAATAACAAAAATTAGCCAGCTTTAGAGAGTGGTGGCACGCTGTAG 4054

QY 387 TCCAGCTACTTGGGAGGCTGAGCGGGAAGATCGCTTGAACCCAGTACAGGAGTTGC 446
Db 4055 TCCAGCGAGTCAGGAGGCTGAGCGAGGAGATCACTGGATCTCGAGGTGGAGGTGC 4114

QY 447 AGTGAGCGGATAGAGTCACTGCACTCCAGCTGGGTGACAGACAGACTCCCTCTC 506
Db 4115 AGTGAGCGGAGAT-GGTACTCTGTACTCCAGCTGGGAGGAGTGGTGGCACGCTGGTCTC 4173

QY 507 AGAAATAAA 516
Db 4174 AAAAAAATAA 4183

RESULT 8

US-08-367-841A-10
Sequence 10, Application US/08367841A
Patent No. 6319687
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Tombran-Tink, Joyce
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,841A
FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7210 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE: Human
IMMEDIATE SOURCE:
LIBRARY: DASH II
FEATURE:
NAME/KEY: JT6A
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: 7.0 kb No. 6319687 1-No. 6319687
OTHER INFORMATION: fragment; derived from human placental
OTHER INFORMATION: genomic DNA; also referred to as JT106
US-08-367-841A-10

Query Match 27.8%; Score 277.8; DB 4; Length 7210;
Best Local Similarity 82.3%; Pred. No. 5.2e-54;
Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;

QY 88 GCCTAGGCGGGTGGCTCAGCGCTGTATATCCAGCACCTTTAGAAAGTGAAGAGGGTGA 147
Db 3756 GCGCGGGCAGCGTGGCTCAGCGCTGTATCCAGCACCTTTGGAGGCCGAGGCGAGA 3815

QY 148 TCACCTTGAAGTCAGGAGTTTTCAGACCGAGCTGGCCACACGCTGTAATCCAGCACCTTTGGG 207
Db 3816 TCACCTTGAAGTCAGGAG-TTCGAGACCGAGCTGGCTTAACACGATGAACCCCGTCTCTAC 3874

QY 208 TAAAAATA-AAAAATTAGCTNGGCGGTGGCTCACACCTGTATATCCAGCACCTTTGGG 266
Db 3875 TAAAAATACAAAAAATTAGCTGGGCGCGGTGGCTGTGCTGTGTATATCCAGCACCTTTGGG 3934

QY 267 AGGCTGAGAGCGGTGGATCCTTGAAGTCAGGAGTTCAAGGCCAGCGCTGGGCAACATGGT 326
Db 3935 AGGCAGAGGTGGGCGAGATCACTTGAAGTCAGGAGTTTGAAGCACGCTAGCCATGGT 3994

QY 327 GAAACCCATCTCTACTAAATAACAAAAATTAGCCAGCTTTAGAGAGTGGTGGCACGCTGTAG 386
Db 3995 GAAACCCATCTCTACTAAATAACAAAAATTAGCCAGCTTTAGAGAGTGGTGGCACGCTGTAG 386

QY 3995 GAAACCCATCTCTACTAAATAACAAAAATTAGCCAGCTTTAGAGAGTGGTGGCACGCTGTAG 4054

QY 387 TCCAGCTACTTGGGAGGCTGAGCGGAGAGATCGCTTGAACCCAGTAGGACAGGTTGC 446
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Db 4055 TCCAGCCAGCTCAGGAGGCTGAGCGAGGAGATCACTGGAATCCTGGAGGTGGAGTTGC 4114
|||||
QY 447 AGTGAGCCGAGATAGAGTCACTGCACTCCAGCTGGGTGACAGAGCAAGACTCCCTCTC 506
|||||
Db 4115 AGTGAGCCGAGAT-GGTACCTCTGTACTCCAGCTGGGGACAGAGTGAAGTCCGCTCTC 4173
|||||
QY 507 AGAATAAATA 516
|||||
Db 4174 AAAAAAAAAA 4183
|||||

RESULT 9

PCT-US95-07201-10
; Sequence 10, Application PC/TUS9507201
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Becerra, Sofia
; APPLICANT: Patricia; Schwartz, Joan P.;
; APPLICANT: Taniwaki, Tekayuki
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMTC
; TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07201
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/367,841
; FILING DATE: 30-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,963
; FILING DATE: 07-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/952,796
; FILING DATE: 24-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36434
; REFERENCE/DOCKET NUMBER: 20264126PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7210 Base Pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Unknown
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; LIBRARY: DASH II
; FEATURE:
; NAME/KEY: JT6A
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: 7.0 kb Not 1-Not
; OTHER INFORMATION: Fragment; Derived from human placental

; OTHER INFORMATION: genomic DNA; also referred to as JT106
PCT-US95-07201-10

Query Match 27.8%; Score 277.8; DB 5; Length 7210;
Best Local Similarity 82.3%; Pred. No. 5.2e-54;
Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;
QY 88 GGCTAGGCGGGTGGCTCAAGCTGTATCCCGACACACTTTAGAGGTGCAAGAGGGTGA 147
|||||
Db 3756 GGCGGGGACGGTGGCTCAAGCTGTATCCCGACACACTTTGGAGGCCGAGGACAGA 3815
|||||
QY 148 TCACCTGAGGTGAGGATTTTGGACACAGCTGGCCACACGGGTGAACCCCATCTCTAC 207
|||||
Db 3816 TCACCTGAGGTGAGGAT-TTCGAGACAGCTGGCTTAACAGATGAACCCGCTCTCTAC 3874
|||||
QY 208 TAAAAATA-AAAAAATTAGCTGGGTGGGTGGCTCACACCTGTAAATCCCGACACTTTGGG 266
|||||
Db 3875 TAAAAATA-CAAAAAATTAGCTGGGTGGGTGGCTGTGCTGTAAATCCCGACACTTTGGG 3934
|||||
QY 267 AGGCTGAGACGGGTGGATCACCTGAAGTCAGGAGTTCAAGGCCAGCTGGGCAACATGGT 326
|||||
Db 3935 AGGCGAGAGGTGGGACATCACTTGAGGTTCAGGAGTTTGAGACCCAGCTAGCCACATGGT 3994
|||||
QY 327 GAAACACACTCTCTACTATAAATAACAAAAATTAGCCAGGTGTGGTGACACAGCTCTAG 386
|||||
Db 3995 GAAACCCCATCTCTACTATAAATACTACAAAAATTAGCCGAGGTGTGGTGACAGCTCTGTA 4054
|||||
QY 387 TCCGAGCTACTTGGGAGGCTGAGCGGAGAGATCGCTTGAACCCAGTAGGCGAGGTTGC 446
|||||
Db 4055 TCCGAGCCAGTCAGGAGGCTGAGCGAGGAGATCACTGGAATCCTTGGAGGTGGAGTGC 4114
|||||
QY 447 AGTGAGCCGAGATAGAGTCACTGCACTCCAGCTGGGTGACAGAGCAAGACTCCCTCTC 506
|||||
Db 4115 AGTGAGCCGAGAT-GGTACCTCTGTACTCCAGCTGGGGACAGAGTGAAGTCCGCTCTC 4173
|||||
QY 507 AGAATAAATA 516
|||||
Db 4174 AAAAAAAAAA 4183
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RESULT 10

US-08-520-373D-4
; Sequence 4, Application US/08520373D
; Patent No. 6451763
; GENERAL INFORMATION:
; APPLICANT: Tombran-Tink, Joyce
; APPLICANT: Steele, Fintan R
; APPLICANT: Chader, Gerald J
; APPLICANT: Becerra, Sofia P
; APPLICANT: Johnson, Lincoln V
; APPLICANT: Rodriguez, Ignacio R
; TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
; FILE REFERENCE: 2026-4203US1
; CURRENT APPLICATION NUMBER: US/08/520,373D
; CURRENT FILING DATE: 1995-08-29
; PRIOR APPLICATION NUMBER: 08/377,710
; PRIOR FILING DATE: 1995-01-25
; PRIOR APPLICATION NUMBER: 08/279,979
; PRIOR FILING DATE: 1994-07-25
; PRIOR APPLICATION NUMBER: 07/894,215
; PRIOR FILING DATE: 1992-06-04
; PRIOR APPLICATION NUMBER: 07/952,796
; PRIOR FILING DATE: 1992-09-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 14581
; TYPE: DNA HUMAN
; ORGANISM:
; FEATURE:
; OTHER INFORMATION: mRNA: 6683; EXON: 6683; EXON: 6683-6790; EXON 11584-11675;
; OTHER INFORMATION: INTRON: 14539-14581; INTRON: 6791-11583; INTRON:
; OTHER INFORMATION: 11676-14538; CDS: 11584-11675; 14539-14580

US-08-520-373D-4

Query Match 27.8%; Score 277.8; DB 4; Length 14581;
Best Local Similarity 82.3%; Pred. No. 5.9e-54;
Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;
QY 88 GGTAGGCGCGGTGCTCAGCGCTGTATCCAGCACTTTAGAGGTGGAAGAGGTGGA 147
Db 3755 GCGCGGCGCGGTGCTCAGCGCTGTATCCAGCACTTTGGAGGCGCGAGGCGAGA 3814
QY 148 TCACITTAGGTGAGGAGTGTGAGACAGCGCTGCGCAACAGCGTGAACCCCATCTCTAC 207
Db 3815 TCACITTAGGTGAGGAGTGTGAGACAGCGCTGCGCAACAGCGTGAACCCCATCTCTAC 3873
QY 208 TAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 266
Db 3874 TAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3933
QY 267 AGGCTGAGCGGTGAGTCACTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 326
Db 3934 AGGCTGAGCGGTGAGTCACTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 3993
QY 327 GAAACACAGCTCTCTACTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 386
Db 3994 GAAACACAGCTCTCTACTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4053
QY 387 TCCAGCTACTTTGGAGGCTGAGGCGGAGAAATCGCTTGAACCCAGTAGGAGGTTCG 446
Db 4054 TCCAGCGAGTCAAGGAGGCTGAGGCGGAGAAATCACTGGAATCTCTGAGGTGAGGTGCG 4113
QY 447 AGTGAGCGAGATAAGAGTCACTGCACTCCAGCGCTGCGTGAACCCAGTAGGAGGTTCG 506
Db 4114 AGTGAGCGAGAT-GGTACTCTGTACTCCAGCGCTGCGGAGGAGAGAGTGAAGTCTCGTCTC 4172
QY 507 AGAAATAAAA 516
Db 4173 AAAAAAATAA 4182

RESULT 11

US-08-367-841A-43
; Sequence 43, Application US/08367841A
; Patent No. 6319687
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Rodriguez,
; APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
; APPLICANT: Tombran-Tink, Joyce
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/367,841A
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,963
; FILING DATE: 07-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/952,796
; FILING DATE: 24-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: PI-147
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: full length genomic
OTHER INFORMATION: sequence for PEDF plus flanking sequences.
US-08-367-841A-43

Query Match 27.8%; Score 277.8; DB 4; Length 22481;
Best Local Similarity 82.3%; Pred. No. 6.4e-54;
Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;
QY 88 GGTAGGCGCGGTGCTCAGCGCTGTATCCAGCACTTTAGAGGTGGAAGAGGTGGA 147
Db 3748 GCGCGGCGCGGTGCTCAGCGCTGTATCCAGCACTTTGGAGGCGCGAGGCGAGCAGA 3807
QY 148 TCACITTAGGTGAGGAGTGTGAGACAGCGCTGCGCAACAGCGTGAACCCCATCTCTAC 207
Db 3808 TCACITTAGGTGAGGAGTGTGAGACAGCGCTGCGCAACAGCGTGAACCCCATCTCTAC 3866
QY 208 TAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 266
Db 3867 TAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3926
QY 267 AGGCTGAGCGGTGAGTCACTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 326
Db 3927 AGGCTGAGCGGTGAGTCACTTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 3986
QY 327 GAAACACAGCTCTCTACTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 386
Db 3987 GAAACACAGCTCTCTACTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4046
QY 387 TCCAGCTACTTTGGAGGCTGAGGCGGAGAAATCGCTTGAACCCAGTAGGAGGTTCG 446
Db 4047 TCCAGCGAGTCAAGGAGGCTGAGGCGGAGAAATCACTGGAATCTCTGAGGTGAGGTGCG 4106
QY 447 AGTGAGCGAGATAAGAGTCACTGCACTCCAGCGCTGCGTGAACCCAGTAGGAGGTTCG 506
Db 4107 AGTGAGCGAGAT-GGTACTCTGTACTCCAGCGCTGCGGAGGAGAGTGAAGTCTCGTCTC 4165
QY 507 AGAAATAAAA 516
Db 4166 AAAAAAATAA 4175

RESULT 12

PCT-US95-07201-43
; Sequence 43, Application PC/TUS9507201
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Becerra, Sofia
; APPLICANT: Patricia; Schwartz, Joan P.;
; APPLICANT: Panikwaki, Takayuki
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07201
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: PL-147
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: full length genomic
OTHER INFORMATION: sequence for PEDF plus flanking sequences.
PCT-US95-07201-43

Query Match 27.8%; Score 277.8; DB 5; Length 22481;
Best Local Similarity 82.3%; Pred. No. 6.4e-54;
Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;

QY 88 GGCTAGGCGCGGTGGCTCAGCGCTGTAATCCCGACACTTTAGAGGTCGAGAGGGTGA 147
DB 3748 GCGCGGCGACGGTGGCTCAGCCCTGTAGTCCCGACACTTTGGGAGCGCGAGGCGAGA 3807

QY 148 TCACCTTAGGTGAGAGTTTGGAGACCGCTGGCCAAACACCGGTGAACCCCATCTCTAC 207
DB 3808 TCACCTTAGGTGAGAG-TTCGAGACCGCTGGCTTAACAGATGAACCCCGTCTCTAC 3866

QY 208 TAAAAATA-AAAAATTAGCTNGGGTGGGTGGCTCAGACTGTATCCAGCACTTTGGG 266
DB 3867 TAAAAATA-AAAAAATTAGTGGGCGACGGTGGCTGTATCCAGCACTTTGGG 3926

QY 267 AGGCTGAGCGGTGGATCAGCTGAAGTCAGAGTTCAAGCCGAGCTGGGCAACATGCT 326
DB 3927 AGGCGAGGTGGGCGAGTCACTTGGGTGAGAGTTTGAACCGCTTAGCCACATGCT 3986

QY 327 GAAACCACTCTCTACTAAAAATA-AAAAAATTAGCCAGGTGTGGTGACACCGCTGTAG 386
DB 3987 GAAACCCCATCTCTACTAAAAATA-AAAAAATTAGCCGAGGTGTGGTGACCGCTGTAA 4046

QY 387 TCCAGCACTTTGGGAGGCTGAGCGGAGAGTCCGTGTAACCCAGTAGGAGGTTGC 446
DB 4047 TCCAGCGCAGTCAGGAGGCTGAGCGGAGAGTCACTGGAATCTTGGAGGTGGG 4106

QY 447 AGTGAGCCGAGATAAGAGTCACTGCACTCCAGCTGGGTGAGAGGAGGAGTCCCTCTC 506
DB 4107 AGTGAGCCGAGAT-GGTACTCTGTACTCCAGCTGGGAGGAGGAGTCCCTCTC 4165

QY 507 AGAATAAATA 516
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DB 4107 AGTGAGCCGAGAT-GGTACTCTGTACTCCAGCTGGGAGGAGGAGTGAAGTCCCTCTC 4165

QY 507 AGAATAAATA 516
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DB 4166 AAAAAAAAAA 4175
|||||

RESULT 13
US-09-875-223-2
Sequence 2, Application US/09875223
Patent No. 6391850
GENERAL INFORMATION:
APPLICANT: No. 6391850thwestern University
APPLICANT: No. 63918501 Bouck
APPLICANT: David Dawson
APPLICANT: Paul Gillis
TITLE OF INVENTION: Methods and Compositions for Inhibiting Angiogenesis
FILE REFERENCE: 0290-2303
CURRENT APPLICATION NUMBER: US/09/875,223
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 09/122,079
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: PCT/US98/15228
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: US 08/899,304
PRIOR FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 22484
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Unsure
LOCATION: 1...22484
OTHER INFORMATION: "n" means either a, c, t, or g
US-09-875-223-2

Query Match 27.8%; Score 277.8; DB 4; Length 22484;
Best Local Similarity 82.3%; Pred. No. 6.4e-54;
Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;

QY 88 GGCTAGGCGCGGTGGCTCAGCGCTGTAATCCCGACACTTTAGAGGTCGAGAGGGTGA 147
DB 3748 GCGCGGCGACGGTGGCTCAGCCCTGTAGTCCCGACACTTTGGGAGCGCGAGGCGAGA 3807

QY 148 TCACCTTAGGTGAGAGTTTGGAGACCGCTGGCCAAACACCGGTGAACCCCATCTCTAC 207
DB 3808 TCACCTTAGGTGAGAG-TTCGAGACCGCTGGCTTAACAGATGAACCCCGTCTCTAC 3866

QY 208 TAAAAATA-AAAAATTAGCTNGGGTGGGTGGCTCAGACTGTATCCAGCACTTTGGG 266
DB 3867 TAAAAATA-AAAAAATTAGTGGGCGACGGTGGCTGTATCCAGCACTTTGGG 3926

QY 267 AGGCTGAGCGGTGGATCAGCTGAAGTCAGAGTTCAAGCCGAGCTGGGCAACATGCT 326
DB 3927 AGGCGAGGTGGGCGAGTCACTTGGGTGAGAGTTTGAACCGCTTAGCCACATGCT 3986

QY 327 GAAACCACTCTCTACTAAAAATA-AAAAAATTAGCCAGGTGTGGTGACACCGCTGTAG 386
DB 3987 GAAACCCCATCTCTACTAAAAATA-AAAAAATTAGCCGAGGTGTGGTGACCGCTGTAA 4046

QY 387 TCCAGCACTTTGGGAGGCTGAGCGGAGAGTCCGTGTAACCCAGTAGGAGGTTGC 446
DB 4047 TCCAGCGCAGTCAGGAGGCTGAGCGGAGAGTCACTGGAATCTTGGAGGTGGG 4106

QY 447 AGTGAGCCGAGATAAGAGTCACTGCACTCCAGCTGGGTGAGAGGAGGAGTCCCTCTC 506
DB 4107 AGTGAGCCGAGAT-GGTACTCTGTACTCCAGCTGGGAGGAGGAGTCCCTCTC 4165

QY 507 AGAATAAATA 516
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; FILE REFERENCE: CL000904
; CURRENT APPLICATION NUMBER: US/09/729,995
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 29629
; TYPE: DNA
; ORGANISM: Human
; US-09-729-995-3

Query Match          27.3%; Score 272.6; DB 4; Length 29629;
Best Local Similarity 79.7%; Pred. No. 1e-52;
Matches 370; Conservative 0; Mismatches 90; Indels 4; Gaps 4;

QY 85 ATAGCTAGCGCGGTGGCTCAGCGCTGTAAATCCACGACACTTTAGAAAGGTTCGAAGAGGGT 144
Db 13877 ATCGGTGAGCGATGTTGGCTGCTGCTGCTGTAAATCCAGCCCTTTGGGAGGCCAAGTAGGT 13936

QY 145 GGATCACTTCAGGTGAGGAGTTTGAGACCAAGCTGGGCCAAACACGCGTGAACCCCATCTC 204
Db 13937 GGATCACTTCAGGTGAGGAG-TTTGAGACCAAGCTGGGCCAAACGTTGTTGAACCCCGTCTC 13995

QY 205 TACT-AAAAATAAAAAATTAGCTNGGGTGGCGGTGGCTCACACCTGTAAATCCAGACACTTT 263
Db 13996 TACTAAAAATAACAAAATTAGCCGGGCATGGTGGCGGCACCTGTAAATTCAGCTACTT 14055

QY 264 GGGAGGCTGAGACGGGTGGATCACTTGAAGTCAGAGAGTTTCAAGGCCACAGCTGGGCCACAT 323
Db 14056 GCGAGGCCGAGGACAGGTGGATCACTTGAGTTCAGAGTTCAGACAGACCTGGCCACAGT 14115

QY 324 GGTGAAACCACCTCTCTACT-AAAAATACAAAATTAGCCAGGTGGTGGTGCGACACGCGCT 382
Db 14116 GGTGAAACCCCGTCTCTACTTAAAAAATACAAAATTAGCCGGGCATGGTGGCGAGCACCT 14175

QY 383 GTAGTCCCACTACTTGGGAGGCTGAGCGGAGAGATCGTTGAACCCAGTAGGACGAGG 442
Db 14176 GTAAATCCAGCTACTTTGGGAGGCTGAGGCGAGAGAAATCGTTGCAACCCAGGAGGAGG 14235

QY 443 TTGCAGGTGAGCGGAGATAAGAGTCACTGCACTCCAGCCTGGGTGCAGAGCAAGACTCCC 502
Db 14236 TTGCAGGTGAGCTAAGAT-CTGTCTATTGCACTCTAGCCTGGGCGACAGAGTGCAGACTCTG 14294

QY 503 TCTCAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 546
Db 14295 TCTGAAAAAAAAGACATACATAATCCAGACCTTATTTTAAA 14338

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Job time : 94 secs

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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 15:31:06 ; Search time 351 Seconds
(without alignments)
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Title: US-09-784-423-32

Perfect score: 1000

Sequence: 1 GGTGTACCTTATCTCTCT.....CAGATGATGACCGCGTGC 1000

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2434939 seqs, 1822278265 residues

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	999	99.9	1000	9	US-09-784-423-32
2	320.2	32.0	7017	10	US-09-764-877-3773
3	320.2	32.0	7017	12	US-10-242-515-3773
4	320.2	32.0	20522	10	US-09-764-877-3774
5	320.2	32.0	20522	12	US-10-242-515-3774
6	311.8	31.2	17588	13	US-10-292-798-1277
7	311.8	31.2	17588	13	US-10-017-161-1603
8	307.2	30.7	31703	12	US-10-085-117-172
9	307.2	30.7	53106	13	US-10-034-650-10
10	307	30.7	174424	10	US-09-967-788A-314
11	307	30.7	174424	13	US-09-960-706-969
12	304.2	30.4	113000	13	US-10-376-566-16
13	303.4	30.3	27087	12	US-10-292-798-1279
14	303.4	30.3	27087	13	US-10-017-161-1605
15	301.4	30.1	174424	10	US-09-967-788A-314

Sequence 969, Appl
Sequence 3, Appl
Sequence 30, Appl
Sequence 11, Appl
Sequence 1349, Ap
Sequence 7789, Ap
Sequence 7789, Ap
Sequence 3, Appl
Sequence 3, Appl
Sequence 3428, Ap
Sequence 22, Appl
Sequence 22, Appl
Sequence 123503,
Sequence 123503,
Sequence 5477, Ap
Sequence 10204, A
Sequence 1003, Ap
Sequence 1, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 34, Appl
Sequence 1, Appl
Sequence 191490,
Sequence 191491,
Sequence 191490,
Sequence 191491,
Sequence 24794, A
Sequence 24794, A
Sequence 363, App

ALIGNMENTS

RESULT 1

US-09-784-423-32
; Sequence 32, Application US/09784423
; Patent No. US20020012924A1
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 MB
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,423
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/018,584
; FILING DATE: 04-Feb-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 32

16 301.4 30.1 174424 13 US-09-960-706-969
17 300.6 30.1 32816 9 US-09-729-094-3
18 300.6 30.1 32816 13 US-10-435-631-3
19 297.6 29.8 2836 12 US-10-108-260A-30
20 297.4 29.7 54000 13 US-09-843-377-11
21 297.2 29.7 24533 10 US-09-764-868-1349
22 296.4 29.6 5281 11 US-09-764-891-7789
23 296.4 29.6 5284 11 US-09-764-891-7788
24 296 29.6 15297 14 US-10-003-295-3
25 293.8 29.4 30350 14 US-10-118-328-3
26 293.8 29.4 99014 10 US-09-880-107-3428
27 292.6 29.3 268685 13 US-10-025-966A-22
28 292.6 29.3 268685 13 US-10-265-071-22
29 292.4 29.2 682 13 US-10-027-632-123503
30 292.4 29.2 682 14 US-10-027-632-123503
31 291.6 29.2 13862 11 US-09-764-891-5477
32 291.6 29.2 13862 11 US-09-764-891-10204
33 291.6 29.2 13862 15 US-10-205-428-1003
34 291.6 29.2 52216 9 US-09-747-810-1
35 291.2 29.1 40645 10 US-09-818-656A-3
36 291.2 29.1 40645 14 US-10-216-441-3
37 291 29.1 26874 13 US-10-004-113-34
38 290.8 29.1 455237 10 US-09-933-267A-1
39 289.8 29.0 650 13 US-10-027-632-191490
40 289.8 29.0 650 13 US-10-027-632-191491
41 289.8 29.0 650 14 US-10-027-632-191490
42 289.8 29.0 650 14 US-10-027-632-191491
43 289.8 29.0 684 13 US-10-027-632-24794
44 289.8 29.0 684 14 US-10-027-632-24794
45 289.8 29.0 3273 9 US-09-764-878-363

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SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Circular
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: no
; IMMEDIATE SOURCE:
; CLONE: S132
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 22
; SEQUENCE DESCRIPTION: SEQ ID NO: 32
US-09-784-423-32

Query Match      99.9%; Score 999; DB 9; Length 1000;
Best Local Similarity 100.0%; Pred. No. 5e-24;
Matches 1000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTGACCTTATCTCTCTGAACTCAGTTTCTCTCATCCGTAATAAGAAAGCTGTAG 60
DB 1 GGTGTGACCTTATCTCTCTGAACTCAGTTTCTCTCATCCGTAATAAGAAAGCTGTAG 60
QY 61 ATTGTGTAAAAAATAAATGAATAGGCTAGGCGGGTGGCTCACGCCCTGTAATCCCA 120
DB 61 ATTGTGTAAAAAATAAATGAATAGGCTAGGCGGGTGGCTCACGCCCTGTAATCCCA 120
QY 121 GCATTTAGAGGTGCGAAGGGTGGATCACTTGAGTCAAGAGTTTGTAGACCAAGCTG 180
DB 121 GCATTTAGAGGTGCGAAGGGTGGATCACTTGAGTCAAGAGTTTGTAGACCAAGCTG 180
QY 181 GCCAACACGGTGAACCCCATCTCTACTAAAAATAAAAAATTAGCTGGTGGT 240
DB 181 GCCAACACGGTGAACCCCATCTCTACTAAAAATAAAAAATTAGCTGGTGGTGGT 240
QY 241 CACACTGTATCCAGCACTTTGGGAGGCTGAGACGGGTGATCACCTGAAGTCAAGAG 300
DB 241 CACACTGTATCCAGCACTTTGGGAGGCTGAGACGGGTGATCACCTGAAGTCAAGAG 300
QY 301 TTCAGGCCAGCTTGGGCAACATGTTGAACACGCTCTTACTAAAAATAAAAAATTAG 360
DB 301 TTCAGGCCAGCTTGGGCAACATGTTGAACACGCTCTTACTAAAAATAAAAAATTAG 360
QY 361 CCAGGTGTGGTGGCACACGCTGTAGTCCAGCTTCTGGGAGGCTGAGCGGAGATC 420
DB 361 CCAGGTGTGGTGGCACACGCTGTAGTCCAGCTTCTGGGAGGCTGAGCGGAGATC 420
QY 421 GCTTGAACCCAGTAGGCGAGGTTGCACTGAGCGGAGATGAGAGTCACTGCATCCAGC 480
DB 421 GCTTGAACCCAGTAGGCGAGGTTGCACTGAGCGGAGATGAGAGTCACTGCATCCAGC 480
QY 481 TGGGTGACAGGCGAAGACTCCCTCTCAGAAATAAATAAATAAATAAATAAATAA 540
DB 481 TGGGTGACAGGCGAAGACTCCCTCTCAGAAATAAATAAATAAATAAATAAATAA 540
QY 541 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 600
DB 541 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 600
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DB 601 AGTAATAGCTATCAATATCCCAACCCCTACCCTGCTGCTGAAATTTAGTTTCTT 660
QY 661 ACCCCCAATTAGACTTAAAGCAGAAATTTCTACCGTACTCTCTGTAATTTCTG 720
DB 661 ACCCCCAATTAGACTTAAAGCAGAAATTTCTACCGTACTCTCTGTAATTTCTG 720
QY 721 GGCACATAGTTGGGTCTCAGTGAACACATGTTGAGTGAATGAGCAATGCAAGGAT 780
DB 721 GGCACATAGTTGGGTCTCAGTGAACACATGTTGAGTGAATGAGCAATGCAAGGAT 780
QY 781 AGGCCATCTGGAGCCCTCCAGCGGGTGGTGGTGGGAACTCATAGTCTCTCTCAAT 840
DB 781 AGGCCATCTGGAGCCCTCCAGCGGGTGGTGGTGGGAACTCATAGTCTCTCTCAAT 840
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QY 841 GGGCCACTGAAGGTAGAGAGTTCTGGGTCCCACTCTCGGACCCCCCATCTCTGACTCAC 900
DB 841 GGGCCACTGAAGGTAGAGAGTTCTGGGTCCCACTCTCGGACCCCCCATCTCTGACTCAC 900
QY 901 TGCTGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960
DB 901 TGCTGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960
QY 961 CAGGACTGCAAGGAGGCCAGCAGAAATGATGACCGCGGTGC 1000
DB 961 CAGGACTGCAAGGAGGCCAGCAGAAATGATGACCGCGGTGC 1000
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RESULT 2

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US-09-764-877-3773/c
; Sequence 3773, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3773
; LENGTH: 7017
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3773
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Query Match      32.0%; Score 320.2; DB 10; Length 7017;
Best Local Similarity 84.6%; Pred. No. 6e-70;
Matches 406; Conservative 0; Mismatches 69; Indels 5; Gaps 4;
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QY 86 TAGGCTAGCGCGGTGGCTCAGCCCTGTAAATCCAGCACTTTAGAGGTGCAAGAGGGTG 145
DB 4509 TGGGCCAGACGGGTGGCTCAGACCTGTATCCAGCACTTTGGAAGCGCGGGTG 4450
QY 146 GATCACTTCAAGTCAGAGGTTTGTAGACACAGCTGGCCACACGGTGAACCCCATCTCT 205
DB 4449 GATCACTTCAAGTCAGAGG-TTCGAGACCAAGCTGGCCACACATGTTGAACCTCTCT 4391
QY 206 ACTAAAAATAAATAAATTAGCTGGTGGTGGTCTACACCTGTAAATCCAGCACTTTGG 265
DB 4390 ACTAAAAATAAATAAATTGACTGGCGCAGTGGTCTACACCTGTATCCAGCACTTTGG 4331
QY 266 GAGGCTGAGACCGGTGGATCACTGAAGTCAGAGGTTCAAGCCAGCTGGGCAACATGG 325
DB 4330 GAGGCCAAGGCGGCAGATCA-TGAGGTCAAGAGATGGAGACCATCTCTGGTAAACATGG 4273
QY 326 TGAACCAAGCTCTCTACTAAAAATAAATAAATTAGCAGGTGTGGTGGCAACGCTGTA 385
DB 4272 TGAACCCGCTCTCTACTAAAAATAAATAAATTAGCCAGCATGGTGGCACACGCTGCA 4213
QY 386 GTCCAGCTACTTGGGAGGCTGAGCGGAGAAATCCCTTGAACCCAGTGAAGCAGAGTTG 445
DB 4212 GTCCAGCTACTTCAAGAGGCTGAGCGAGGAAATAGCCCTGAACCCAGGAGCGAGTTG 4153
QY 446 CAGTGAGCGGAGATGAGTCACTGCTCACTCCAGCTGGGTGGTGGTGGTGGTGGTGGT 505
DB 4152 CAGTGAGCGGAGATCA-CGACACTGCTCTCCAGCTGGGCAACGAGCGAGATCCGCT 4094
QY 506 CAGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 565
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RESULT 3

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US-10-242-515-3773/c
; Sequence 3773, Application US/10242515
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Publication No. US20040009488A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005C1
CURRENT APPLICATION NUMBER: US/10/242,515
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/764,877
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3773
LENGTH: 7017
TYPE: DNA
ORGANISM: Homo sapiens
US-10-242-515-3773

Query Match 32.0%; Score 320.2; DB 12; Length 7017;
Best Local Similarity 84.6%; Pred. No. 6e-70;
Matches 406; Conservative 0; Mismatches 59; Indels 5; Gaps 4;
QY 86 TAGCTAGGCGGGTGGCTCAACCTGTAATCCAGCAGCTTTAGAGAGTTCAGAGGGTG 145
DB 4509 TGGGCCAGACGGGTGGCTCACCTGTTATCCAGCAGCTTTGGAAGCGGCGGGTG 4450
QY 146 GATCAGCTGAGCTCAGAGTTTGAACACAGCTTGGCCACACGGTGAAACCCCATCTCT 205
DB 4449 GATCAGCTGAACACAGAG-TTCGAGACAGCTGGCCACATGGTGAAACCTGCTCT 4391
QY 206 ACTAAAAATAAAAAATTAGCTNGGCTGGCTCACCTGTAATCCAGCAGCTTTAGAGAGTTCAGAGGGTG 145
DB 4390 ACTAAAAATACAAAAATTGACTGGCGCAGTGGCTCACCTGTTACCCAGCAGCTTTGG 265
QY 266 GAGCTGACAGCGGTGGATCACCTGAAGTCAAGAGTTCAGAGCGAGCTGGGCAACATGG 325
DB 4330 GAGGCCAAGCGGCGAGATCA--TGAGGTCAAGAGATGGAGACCATCTGGCTAACATGG 4273
QY 326 TGAACACCGCTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGGCAGCCCTGTA 385
DB 4272 TGAACACCGCTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGGCAGCCCTGTA 4213
QY 386 GTCCAGCTACTTGGGAGGCTGAGCGGAGAAATCGCTTGAACCCAGTGGCAGAGTTG 445
DB 4212 GTCCAGCTACTCAGGAGGCTGAGCGAGAGATAGCTTGAACCCAGGAGGAGTTG 4153
QY 446 CAGTGAAGCAGAGTAAGAGTCACTGCTCCAGCTGGGTGACAGAGCAAGATCCCTCT 505
DB 4152 CAGTGAAGCAGAGTCA-CGACACTGCTCCAGCTGGGCAACAGAGGAGATCCGCT 4094
QY 506 CAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 565
DB 4093 CA-AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4035

RESULT 4

US-09-764-877-3774/c
Sequence 3774, Application US/09764877
Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3774
LENGTH: 20522
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-877-3774

Query Match 32.0%; Score 320.2; DB 10; Length 20522;
Best Local Similarity 84.6%; Pred. No. 9.8e-70;
Matches 406; Conservative 0; Mismatches 69; Indels 5; Gaps 4;
QY 86 TAGGCTAGGCGCGGTGGCTCAGCCTGTATATCCAGCAGCTTTAGAGAGTTCAGAGGGTG 145
DB 10327 TGGGCCAGACGGGTGGCTCACCTGTTATCCAGCAGCTTTGGAGCGGCGGGTG 10268
QY 146 GATCAGCTTGAAGTCAGAGTTTGAACACAGCTTGGCAGAGCTGGCAGAGTGAACCCCATCTCT 205
DB 10267 GATCAGCTGAAGCAAGG-TTCGAGACAGCCTGGCCCAACATGTTGAAACCTCGTCTCT 10209
QY 206 ACTAAAAATAAAAAATTAGCTNGGCTGGCTGGCTCAGCAGTTCAGAGCGAGCTGGGCAACATGG 325
DB 10208 ACTAAAAATACAAAAATTGACTGGCGCAGTGGCTCACCTGTTACCCAGCAGCTTTGG 10149
QY 266 GAGGCTGAGAGCGGTGGATCAGCTGAAAGTCAGAGTTCAGAGCGAGCTGGGCAACATGG 10091
DB 10148 GAGGCCAAGCGGCGAGATCA--TGAGGTCAAGAGATGGAGACCATCTGGCTAACATGG 10091
QY 326 TGAACACCGCTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGGCAGAGCTGTA 385
DB 10090 TGAACACCGCTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGGCAGAGCTGTA 10031
QY 386 GTCCAGCTACTTGGGAGGCTGAGCGGAGAAATCGCTTGAACCCAGTGGCAGAGTTG 445
DB 10030 GTCCAGCTACTCAGAGGCTGAGCGAGAGATAGCTTGAACCCAGGAGGAGTTG 9971
QY 446 CAGTGAAGCAGAGTAAGAGTCACTGCTCCAGCTGGGTGACAGAGCAAGATCCCTCT 505
DB 9970 CAGTGAAGCAGAGTCA-CGACACTGCTCCAGCTGGGCAACAGAGCGAGATCCCTCT 9912
QY 506 CAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 565
DB 9911 CA-AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 9853

RESULT 5

US-10-242-515-3774/c
Sequence 3774, Application US/10242515
Publication No. US20040009488A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005C1
CURRENT APPLICATION NUMBER: US/10/242,515
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/764,877
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886

;; PRIOR FILING DATE: 2000-06-28
;; PRIOR APPLICATION NUMBER: 60/217,487
;; PRIOR FILING DATE: 2000-07-11
;; PRIOR APPLICATION NUMBER: 60/225,758
;; PRIOR FILING DATE: 2000-08-14
;; PRIOR APPLICATION NUMBER: 60/220,963
;; PRIOR FILING DATE: 2000-07-26
;; PRIOR APPLICATION NUMBER: 60/217,496
;; PRIOR FILING DATE: 2000-07-11
;; PRIOR APPLICATION NUMBER: 60/225,447
;; PRIOR FILING DATE: 2000-08-14
;; PRIOR APPLICATION NUMBER: 60/218,290
;; PRIOR FILING DATE: 2000-07-14
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 4031
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 3774
;; LENGTH: 20522
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-242-515-3774

Query Match 32.0%; Score 320.2; DB 12; Length 20522;
Best Local Similarity 84.6%; Pred. No. 9.8e-70;
Matches 406; Conservative 0; Mismatches 69; Indels 5; Gaps 4;

QY 86 TAGGCTAGGCGGGTGGCTCACGCTGTAAATCCAGCACTTTAGAGGTGGAAGAGGGTG 145
Db TGGGCGAGAGCGGGTGGCTCACACCTGTATCCAGCACTTTGGAAGCCGAGCGGGTG 10268

QY 146 GATCACTTGAAGTCAAGAGTTTGAAGCAGCGCTGGCCACACAGGTGAAACCCCATCTCT 205
Db GATCACTTGAAGCAAGAG-TTCGAGACGAGCGCTGGCCACACATGGTGAACCTGCTCTCT 10209

QY 206 ACTAAATAAATAAATAGCTGGGTGGGTGGCTCACACCTGTAAATCCAGCACTTTGG 265
Db ACTAAATAAATAAATTTGACTGGGCGAGTGGCTCACACCTGTAAATCCAGCACTTTGG 10149

QY 266 GAGGCTGAGACGGGTGGATCACCTGAAGTCAGAGTTCAGGCGCAGCTGGGCAACATGG 325
Db GAGGCGAAGCGGGCGAGATCA--TGAGGTGAGAGATGGAGACCATCTGCTTAACATGG 10091

QY 326 TGAACACAGTCTTACTTAAATAAATAAATAGCAGGTGGTGGTGGCAACGCTGTA 385
Db TGAACCCCGTCTCTACTTAAATAAATAAATAAATAGCAGGTGGTGGTGGCAACGCTGTA 10031

QY 386 GTCCAGCTTACTTGGAGGCTGAGGCGGAGATCGCTTGAACCCAGTGAAGAGGTG 445
Db GTCCAGCTTACTTGGAGGCTGAGGCGGAGATAGCTTGAACCCAGGCGGAGGTG 9971

QY 446 CAGTGAGCGAGATAAGAGTCACTGCTCAGCTCCAGCTGGGTGACAGAGCAAGACTCCCTCT 505
Db CAGTGAGCGAGATCA-CGACACTGCTCAGCTCCAGCTGGGCGACAGAGGAGATCCGCTCT 9912

QY 506 CAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 565
Db CA-AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 9853

RESULT 6

US-10-292-798-1277/c
; Sequence 1277, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABEURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161

;; PRIOR FILING DATE: 2001-12-18
;; PRIOR APPLICATION NUMBER: JP 2001-246789
;; PRIOR FILING DATE: 2001-06-18
;; NUMBER OF SEQ ID NOS: 2070
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1277
;; LENGTH: 17588
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; LOCATION: source
;; FEATURE:
;; LOCATION: (1)..(17588)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (201)..(386)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (560)..(873)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (2637)..(3270)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (3360)..(3460)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (12023)..(12329)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (17307)..(17388)
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (6225)..(6324)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (12380)..(12479)
;; OTHER INFORMATION: a, t, c, g, unknown or other
US-10-292-798-1277

Query Match 31.2%; Score 311.8; DB 12; Length 17588;
Best Local Similarity 80.6%; Pred. No. 1.2e-67;
Matches 400; Conservative 0; Mismatches 93; Indels 3; Gaps 3;

QY 61 ATTGTTGTAATAAATAAATGAATAGCTAGGCGGGTGGCTCACGCTGTAAATCCCA 120
Db TTTGTTGTAATAAATAAATGAATAGCTAGGCGGGTGGCTCACATCTGTAAATCCCA 15229

QY 121 GCATTTAGAGTTCGAGAGGGTGGATCAGTTCAGGTGAGGAGTTTGGAGCGAGCTG 180
Db GCATTTGAGGCGCAAGTGGTGGATCAGTTCAGGCGCAGGAG-TTTGAGCGAGCTG 15170

QY 181 GCCAACACGCTGAAACCCCATCTCTACTAAAAATAAAAAATAGCTGGGTGGGTGGCT 240
Db GCCAACATGCGCAACATCTCTCTACTAAAAATAAAAAATAGCTGGGTGGGTGGCT 15110

QY 241 CACACCTGTAATCCCAACATTTGGGAGGCTGAGACGGGTGGATCACCTGAAGTCAGGAG 300
Db CACACCTGTAATCCCAACATTTGGGAGGCGGAGGGGGGATTAACCTGAGGTTCAGGAG 15109

QY 301 TTCAAGGCGAGCTGGGCAACATGGTGAACACAGCTCTCTACTAAAAATAAAAAATAG 360
Db TTCAAGACCATGTTGGCCAAATATGGTGAACCCCATCTCTCTAAAAATAAAAAATAG 15049

QY 361 CCAGGTGTGGGACACGCTGTAGTCCAGCTTCTTGGGAGGCTGAGGCGGAGCAATC 420
Db CCGGTTGTGGGACACGCTGTAAATCCAGCTATATGGGAGGCTGAGGCGAGAGATC 14930

QY 421 GCTTGAACCGAGTAGGCGAGGTTCAGTGAAGCGAGATAAGAGTCACTCCAGCC 480
Db ACTTGAACCGAGGAGGAGGTTCAGTGAAGCGAGAT-CTCGCCACTGCACTCCAGCC 14871

QY 481 TGGGTGACAGCAGCAGCTCCCTCTCAGAAATATAAATAAATAAATAAATAAATAA 540
Db 14870 T-GGCAACAGAGCAGCAGCTCTGTCTCAAAATAAATAAATAAATAAATAAATA 14812
QY 541 AATAAAATAAATAA 556
Db 14811 AATAAATAAATAAATAA 14796

RESULT 7
US-10-017-161-1603/c
; Sequence 1603, Application US/10017161
; Publication No. US2003014368A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1603
; LENGTH: 17588
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(17588)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(386)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (660)..(873)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2637)..(3270)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3360)..(3460)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12023)..(12329)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17307)..(17388)
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (6225)..(6324)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (12380)..(12479)
; OTHER INFORMATION: a, t, c, g, unknown or other

Query Match 31.2%; Score 311.8; DB 13; Length 17588;
Best Local Similarity 80.6%; Pred. No. 1.2e-67;
Matches 400; Conservative 0; Mismatches 93; Indels 3; Gaps 3;

QY 61 ATTGTTGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 120
Db 15288 ATTGATTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 15229
QY 121 GCATTAGAGAGGTCGAAGAGGAGGATCACTTAGGTGAGGAGGAGGAGGAGGAG 180
Db 15228 GCATTGCGAGGCGAAAGTGGTGGATCACTTAGGCGCAGAG-TTTAGACCGCCTG 15170

QY 181 GCCAACAGGTGAACCCCATCTCTACTAAAAATAAAAAATTAGCTNGGTCGGTGGCT 240
Db 15169 GCCACATGGCAAACTCTGTCTCTACTAAAAATACAAAATTGCTGGCGCAGTAGCT 15110
QY 241 CACACCTGTAATCCAGCAGCTTTGGGAGGCTGAGACGGGTGATCACCTGAAGTCAGGAG 300
Db 15109 CACACCTGTAATCCACACCTTTGGAGGCGGCGCGGATTTACCTGAGGTGAGGAG 15050
QY 301 TTCAAGGCCAGCTGGGCAACATGGTGAACCAACGCTCTCTACTAAAAATAAAAAATTAG 360
Db 15049 TTCAAGACCACTGTGGCCAATATGTTGAACCCCATCTCTACTAAAAATAAAAAATTAG 14990
QY 361 CCAGGTGTGGTGGCAGACGCTGTAGTCCCGAGCTACTTGGGAGGCTGAGCGGAAGATC 420
Db 14989 CCGGGTGTGGTGGCAGACGCTGTAGTCCCGAGCTACTTGGGAGGCTGAGCGGAAGATC 14930
QY 421 GCTTGAACCCAGTAGGAGGTTGCAGTGCAGCGCAGAGATAAGAGTCACTCTCATCCAGCC 480
Db 14929 ACTTGAACCCAGGAGGAGGAGGTTGCAGTGCAGCGCAGAT-CTCGCCTGCTCGAGCC 14871
QY 481 TGGGTGACAGCAGCAGCTCCCTCTCAGAAAAATAAATAAATAAATAAATAAATAA 540
Db 14870 T-GGCAACAGAGCAGCAGCTCTGTCTCAAAATAAATAAATAAATAAATAAATAA 14812
QY 541 AATAAAATAAATAA 556
Db 14811 AATAAATAAATAAATAA 14796

RESULT 8
US-10-085-117-172/c
; Sequence 172, Application US/10085117
; Publication No. US2003023234A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric X.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 172
; LENGTH: 31703
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)..(31703)
; OTHER INFORMATION: n = any nucleotide
US-10-085-117-172

Query Match 30.7%; Score 307.2; DB 12; Length 31703;
Best Local Similarity 80.6%; Pred. No. 2.2e-66;
Matches 407; Conservative 0; Mismatches 94; Indels 4; Gaps 4;

QY 47 TGAAGAAGCTGTAGATTGTTGTAATAAATAAATAAATAAATAAATAAATAAATAA 106
Db 3753 TGACAGAGTGAGACCCCTTTAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 3694
QY 107 CGCTGTATATCCCGACCTTTAGAGGTGCGAAGGCGGTGATCATCTTAGGTGAGAGTT 166
Db 3693 CACCTGTATATCCCGACCTTTAGAGGCGGCGGCTGTGAT-ACCTGAGGCCAGAG-T 3636
QY 167 TTGAGACCAAGCTGGCCCAACAACGGTGAACCCCATCTCTACTAAAAATA-AAAAATTAG 225
Db 3635 TGGAGACCAAGCTGGCAACAATGGTGAACCCCATCTTACTAAAAATAAATAAATTAG 3576
QY 226 TNGGGTGGCGGTGCTACACCTGTATATCCAGCAGCTTTGGGAGGCTGAGACGGGTGATC 285
Db 3575 CCAGGCAAGTGGTGTACACCTGTATATCCAGCAGCTTTGGGAAGCTGTGGCGGCGAGTC 3516

QY 286 ACTGAAGTCAGGAGTTCAGGCGCAGCTGGGCAACATGCTGAACACGCTCTCTAA 345
Db |||||
QY 346 AATATCAAAAATAGCAGAGTGTGGGCAACGCGCTGTAGTCCAGCTACTTTGGGAGGC 405
Db |||||
QY 3455 AATATCAAAAATAGCAGAGTGTGGGCAACGCGCTGTAGTCCAGCTACTTTGGGAGGC 3396
Db |||||
QY 406 TGAGGCGGGAAGTCTGTGAACCCAGTAGGAGGCTTCCAGTCCAGGAGGATAGAGT 465
Db |||||
QY 3395 TGAGCAGGATATGCTTGAACCCAGGAGGAGGATGAGTCCAGTCCAGGAGGATCA-CGC 3337
Db |||||
QY 466 CACTGCACTCCAGCTGGGTGACAGAGCAAGACTCCCTCTCAGAAAAATAAATAAATA 525
Db |||||
QY 3336 CACTGCACTCCAGCTGGGTGACAGAGTCCAGCTCTCAAAAAAATAAATAAATAA 3277
Db |||||
QY 526 AATAAATAAATAAATAAATAAATAA 550
Db |||||
QY 3276 AAAAAAGAAAAAGAAAAACAAA 3252
Db |||||
RESULT 9
US-10-034-650-10
; Sequence 10, Application US/10034650
; Publication No. US20030216558A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000128
; CURRENT APPLICATION NUMBER: US/10/034,650
; PRIOR FILING DATE: 2002-07-23
; PRIOR FILING DATE: 1999-12-29
; PRIOR FILING DATE: 1999-12-29
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 53106
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-034-650-10
Query Match 30.7%; Score 307.2; DB 13; Length 53106;
Best Local Similarity 77.7%; Pred. No. 2.8e-66;
Matches 408; Conservative 0; Mismatches 114; Indels 3; Gaps 3;
QY 69 AAAAAAATTAATGAATAGCTAGGCGCGGTGGCTCAGCGCTGTAAATCCAGCACTTTA 128
Db |||||
QY 4598 AACCAAAAGACATCTGTGGATGGGCAAGTGGCTCATGCTATATCCCAACATTTG 4657
Db |||||
QY 129 GAAGTCGAGAGGTGATCAGTTCAGGTCAGGATTTTGAACAGCGCTGGGCAACAC 188
Db |||||
QY 4658 GAGGCTGAGTGGGATGATCAGTTCAGGTCAGGAG-TTTGAGCAGCGCTGGCAACAT 4716
Db |||||
QY 189 GGTGAACCCCATCTCTACTAAAAATA-AAAAATTAGCTNGGGTGGGTGCTCAGCCT 247
Db |||||
QY 4717 GTTGAACCCCATCTCTACTAAAAACACAAAAATTAGTGGGATGGTGGCTATCGCT 4776
Db |||||
QY 248 GTATATCCAGCATTTGGGAGGTGAGCAGGATGATCACTGAAGTCAGGAGTTCAAGG 307
Db |||||
QY 4777 GTATATCCAGCATTTGGGAGGTGAGCAGGATGATCACTGAAGTCAGGAGTTCCAGA 4836
Db |||||
QY 308 CAGCCTGGGCAACATGTTGAACCCAGCTCTCTACTAAAAATAAATAAATAAATAA 367
Db |||||
QY 4837 GAGTCTGGGCAACATGTTGAACCCCATCTCTATTAATAAATAAATAAATAAATAA 4896
Db |||||
QY 368 TGGTGGCAGACGCTGTAGTCCAGCTACTTGGGAGGTGAGCGGAGAGATCCCTTGA 427
Db |||||
QY 4897 TGGTGGCAGCTCTCTGTAGTCCCGGCTTCTCAGGAGGTGAGGAGGAGATCACTTGA 4956
Db |||||

QY 428 CCCAGTAGGAGGAGTTCAGTCCAGGAGATAGAGTCACTGCTCCAGCCTGGGTGA 487
Db |||||
QY 4957 CCCAGTAGGAGGAGTTCAGTCCAGGAGATAGAGTCACTGCTCCAGCCTGGGTGA 5015
Db |||||
QY 488 CAGAGCAGAGCTCCCTCTCAGAAAAATAAATAAATAAATAAATAAATAAATAA 547
Db |||||
QY 5016 CAGAGGAGAGCTCCCTCTCAGAAAAATAAATAAATAAATAAATAAATAAATAA 5075
Db |||||
QY 548 TAAATATAAATTTCTAAAGGCTGGCATTTGCTTAGCAGCTTATAT 592
Db |||||
QY 5076 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5120
Db |||||
RESULT 10
US-09-967-768A-314/c
; Sequence 314, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 314
; LENGTH: 174424
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-768A-314
Query Match 30.7%; Score 307; DB 10; Length 174424;
Best Local Similarity 83.1%; Pred. No. 5.5e-66;
Matches 409; Conservative 0; Mismatches 76; Indels 7; Gaps 5;
QY 76 TTAATGAATAGCTAGGCGCGGTGGCTCAGCGCTGTAAATCCAGCACTTTAGAGGTC 135
Db |||||
QY 132168 TAAAAAATAAAGAGTGGCGAGTGGCTCACACCTATATCTTAGCCTTTGGGAGGC 132109
Db |||||
QY 136 GAAGAGGTGGATCAGTTCAGTTCAGGAGTTTGAACAGCGCTGGCCACACAGCTGAAA 195
Db |||||
QY 132108 GAGGAGGTGGATCAGTTCAGTTCAGGAG-TTTGAGCAGCGCTAGCAATGGTGAAA 132050
Db |||||
QY 196 CCCATCTCTACTAAAAAT--AAAAATTAGCTNGGGTGGGTGCTCAGCCTGTAAAT 252
Db |||||
QY 132049 CCCCCTCTCTACCAAAAAATACAAAAAATTAGCGGGGACGCTGGCTCAGCCTATAT 131990
Db |||||
QY 253 CCCAGCATTTGGGAGGCTGAGAGGCTGATCAGTTCAGTTCAGGAGTTCAAGGCCAGC 312
Db |||||
QY 131989 CCAACATTTGGGAGGAGGAGGCGGTGGATCAGTTCAGGTCAGGAGTTCCAGCAGT 131930
Db |||||
QY 313 CTGGGCAACATGCTGAACACAGCTCTCTACTAAAA-ATACAAAAATTCAGCAGGTGGT 371
Db |||||
QY 131929 CTGGCCACATGCTGAACCTCTCTCTCAAAAAATACAAAAAATACCAAGGCGTGGT 131870
Db |||||
QY 372 GGCACAGCTGTAGTCCAGCTACTTTGGGAGGCTGAGCGGAGAGATCGCTTGAACCCA 431
Db |||||
QY 131869 GCGCAGCGCTGTAAATCCAGCTACTTTGGGAGGCTGAGCGGAGAGTTCCTGACCCA 131810
Db |||||
QY 432 GTAGCAGAGTTGAGTTCAGGAGGCTGAGAGTTCAGTTCAGCCTCCAGCCTGGGTGACAG 491
Db |||||
QY 131809 GGAGCAGAGTTGAGTTCAGGAGGCTGAGAGTTCAGGAGGCTGAGGAGGCTGAGGAGG 131751
Db |||||
QY 492 GCAAGATCTCCTCTCAG-AAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 550
Db |||||

NAME/KEY: source
LOCATION: (1)..(27087)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(498)
FEATURE:
NAME/KEY: CDS
LOCATION: (834)..(923)
FEATURE:
NAME/KEY: CDS
LOCATION: (7389)..(7511)
FEATURE:
NAME/KEY: CDS
LOCATION: (10905)..(11021)
FEATURE:
NAME/KEY: CDS
LOCATION: (13053)..(13140)
FEATURE:
NAME/KEY: CDS
LOCATION: (19148)..(19452)
FEATURE:
NAME/KEY: CDS
LOCATION: (26643)..(26887)
US-10-017-161-1605

Query Match
Best Local Similarity 30.3%; Score 303.4; DB 13; Length 27087;
Matches 383; Conservative 0; Mismatches 77; Indels 4; Gaps 3;

QY 86 TAGCTAGGCGGCTGCTACGCTGTAATCCAGCAGCTTTAGAGGTCGAGAGGTTG 145
Db TGGGCCAGGTGGGTGGCCACGCTGTAATCCAGCAGCTTTGGAGGCTTAGAGGCG 8576

QY 146 GATCACTTAGGTGAGGTTTGGAGCCAGCTGGCCCAACAGCGTGAACCCCATCTCT 205
Db GATCACTTAGGTGAGGTTTGGAGCCAGCTGGCCCAACAGCGTGAACCCCATCTCT 8517

QY 206 ACTAAAAATAAAATTAAGCTGGGTGGCTGCTCAGCTGATGTAATCCAGCAGCTTTGG 265
Db ACTAAAAATAAAATTAAGCTGGGTGGCTGCTCAGCTGATGTAATCCAGCAGCTTTGG 8457

QY 266 GAGCTGAGACGGGTGGATCACCTGAGTCAAGGCTCAAGGCGAGCTGGGCAACATGG 325
Db GAGCGCGAGGCGAGGAGATCA--TGAGGTGAGGAGTTCAGACCGAGCTGACCAACATAG 8399

QY 326 TGAAACACGCTCTCTACTAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 385
Db GGAACCCCGTCTCTACTAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 8339

QY 386 GTCCAGCTACTTGGAGGCTGAGGCGGAGNATCGCTTGAACCCAGTGGAGGAGTTG 445
Db GTCCAGATCTCAGGAGTTGAGGCGAGGAGATCGCTTGAACCTGGAGGCGAGGTTG 8279

QY 446 CAGTGGCGAGATAAGAGTCACTGCTCCAGCTGGGTGACAGACAGCTCCCTCT 505
Db CAGTGGCGAGAT--AGCTCCACTGCTCCAGCTGGGTGACAGACAGCTCTGCTCT 8220

QY 506 CAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 549
Db CAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 8176

RESULT 15

US-09-967-768A-314
Sequence 314, Application US/09967768A
Patent No. US20020150877A1
GENERAL INFORMATION:
APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE OF INVENTION: Sets
FILE REFERENCE: 689290-72
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,111
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 325
SOFTWARE: PatentIn version 3.0
SEQ ID NO 314
LENGTH: 174424
TYPE: DNA
ORGANISM: Homo sapiens
US-09-967-768A-314

Query Match
Best Local Similarity 30.1%; Score 301.4; DB 10; Length 174424;
Matches 397; Conservative 0; Mismatches 82; Indels 7; Gaps 4;

QY 70 AAAAAATAAATGGAATAGGCTAGGCGGCTGAGCTCAGCGCTGTAAATCCAGCAGCTTTAG 129
Db AAAAAATAAATGGAATAGGCTAGGCGGCTGAGCTCAGCGCTGTAAATCCAGCAGCTTTAG 69774

QY 130 AAGGTCGAAGAGGCTGATCACTTGAAGTCAGGAGTTTGGAGCAGCAGCTGGCCACG 189
Db AAGGTCGAAGAGGCTGATCACTTGAAGTCAGGAGTTTGGAGCAGCAGCTGGCCACG 69833

QY 190 GTGAACCCCATCTCTACTAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 246
Db GTGAACCCCATCTCTCTACTAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 69893

QY 247 TGTAAATCCAGCAGCTTTGGAGGCTGAGACGGGTGATCACTCAAGTCAGGAGTTCAAG 306
Db TGTAAATCCAGCAGCTTTGGAGGCTGAGACGGGTGATCACTCAAGTCAGGAGTTCAAG 69953

QY 307 GCGAGCTGGGCAACATGTTGAAACCAACGCTCTCTACTAAAAATAAATAAATAAATAAATAA 366
Db ACCAGCTGGACAAATATGTTGAAACCAACGCTCTCTACTAAAAATAAATAAATAAATAAATAA 70013

QY 367 GTGTGGCACAACGCTGTAGTCCAGCTACTTGGAGGCTGAGCGGAGATCGCTTGA 426
Db GTGTGGCGGCGACCTGTAGTCCAGCTACTTGGAGGCTGAGCGGAGATCGCTTGA 70073

QY 427 ACCAGTAGGCGAGGTTGAGTGGAGGCTGAGCGGAGATAGAGTCACTGCACTCCAGCTGGGTG 486
Db ACCTGGGCGAGAGGTTGAGTGGAGGCTGAGCGGAGAT--TGCGCCACTGCACTCTAGCTGGGCG 70132

QY 487 ACAGAGCAAGCTCCCTCTCAGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 546
Db ACAGAGAAAGAGTCTGCTCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 70190

QY 547 AAAAA 552
Db 70191 TAAAAA 70196

Search completed: January 31, 2004, 17:25:56
Job time : 355 secs

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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 17:18:36 ; Search time 38.5 Seconds
(without alignments)
286.612 Million cell updates/sec

Title: US-09-784-423-124

Perfect score: 25

Sequence: 1 GGTTCGAGTGGCCGAGATAAGT 25

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	3	US-09-018-584A-124
2	25	100.0	1000	3	US-09-018-584A-32
3	20	80.0	764	4	US-09-288-143-57
4	20	80.0	1875	2	US-08-683-743-3
5	20	80.0	4042	3	US-08-406-030A-17
6	20	80.0	4129	2	US-08-370-319C-12
7	20	80.0	4129	3	US-09-224-834-12
8	20	80.0	45716	4	US-08-965-048-5
9	20	80.0	45989	4	US-08-965-048-6
10	19	76.0	21	1	US-08-133-623-2
11	19	76.0	239	2	US-08-687-080-93
12	19	76.0	265	2	US-08-849-701-1
13	19	76.0	283	4	US-08-579-445-26
14	19	76.0	294	2	US-08-481-658B-61
15	19	76.0	294	2	US-08-477-504A-61
16	19	76.0	294	2	US-08-486-756A-61
17	19	76.0	294	2	US-08-485-862B-61
18	19	76.0	294	3	US-08-787-739-61
19	19	76.0	294	3	US-08-487-077A-61
20	19	76.0	294	3	US-08-485-863A-61
21	19	76.0	294	3	US-08-485-049D-61
22	19	76.0	294	3	US-09-178-115-61
23	19	76.0	294	3	US-09-177-776-61
24	19	76.0	302	2	US-08-849-701-3
25	19	76.0	308	4	US-09-702-705-1111
26	19	76.0	308	4	US-09-736-457-1111
27	19	76.0	336	3	US-09-385-982-17

c 28 19 76.0 363 4 US-09-702-705-878
c 29 19 76.0 363 4 US-09-736-457-878
c 30 19 76.0 364 4 US-09-702-705-867
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33 19 76.0 367 4 US-09-702-705-1143
34 19 76.0 367 4 US-09-736-457-1626
35 19 76.0 367 4 US-09-736-457-1626
c 36 19 76.0 368 4 US-09-702-705-1003
37 19 76.0 368 4 US-09-702-705-1003
c 38 19 76.0 368 4 US-09-702-705-1038
c 39 19 76.0 368 4 US-09-702-705-1044
c 40 19 76.0 368 4 US-09-702-705-1092
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c 42 19 76.0 368 4 US-09-736-457-1003
c 43 19 76.0 368 4 US-09-736-457-1038
c 44 19 76.0 368 4 US-09-736-457-1044
c 45 19 76.0 368 4 US-09-736-457-1092
Sequence 1584, Ap

ALIGNMENTS

RESULT 1
US-09-018-584A-124
; Sequence 124, Application US/09018584A
; Patent No. 6238863
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; TITLE OF INVENTION: REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; FILING DATE: 04-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 124:
; LENGTH: 25
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-09-018-584A-124

Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 5,7e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGTTCGAGTGGCCGAGATAAGT 25
Db 1 GGTTCGAGTGGCCGAGATAAGT 25

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RESULT 2
US-09-018-594A-32
; Sequence 32, Application US/09018584A
; Patent No. 6238863
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
; TITLE OF INVENTION: REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/018,584A
; FILING DATE: 04-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Circular
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: no
; IMMEDIATE SOURCE:
; CLONE: S132
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 22
; US-09-018-594A-32

Query Match 100.0%; Score 25; DB 3; Length 1000;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCGAGATAAGGT 25
Db 441 GGTTCAGTGCAGCGAGATAAGGT 465

RESULT 3
US-09-288-143-57
; Sequence 57, Application US/09288143
; Patent No. 6433139
; GENERAL INFORMATION:
; APPLICANT: Brewer et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P1
; CURRENT APPLICATION NUMBER: US/09/288,143
; CURRENT FILING DATE: 1999-04-08
; EARLIER APPLICATION NUMBER: PCT/US98/21142
; EARLIER FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 60/061,463
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,529

Query Match 90.0%; Score 20; DB 2; Length 1875;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/071,498
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,527
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,536
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,532
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 764
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-288-143-57

Query Match 80.0%; Score 20; DB 4; Length 764;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCGAGATA 20
Db 674 GGTTCAGTGCAGCGAGATA 693

RESULT 4
US-08-683-743-3
; Sequence 3, Application US/08683743
; Patent No. 5843697
; GENERAL INFORMATION:
; APPLICANT: Pestka, Sidney
; APPLICANT: Kotsenko, Serguei
; TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
; TITLE OF INVENTION: CHAIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,743
; FILING DATE: 17-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 601-1-050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1875 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; US-08-683-743-3
```


QY 1 GGTTCAGTGAGCCGAGATA 20
DB 1551 GGTTCAGTGAGCCGAGATA 1570

RESULT 5

US-08-406-030A-17
; Sequence 17, Application US/08406030A
; Patent No. 6270989
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Hauge, Brian M.
; APPLICANT: Seliden, Richard F.
; TITLE OF INVENTION: Protein Production and Delivery
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,030A
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/243,391
; FILING DATE: 13-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,586
; FILING DATE: 03-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,533
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,840
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,188
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11704
; FILING DATE: 02-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09627
; FILING DATE: 05-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: TKT95-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4042 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-406-030A-17

Query Match 80.0%; Score 20; DB 3; Length 4042;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
DB 2894 GGTTCAGTGAGCCGAGATA 2913

RESULT 6

US-08-370-319C-12
; Sequence 12, Application US/08370319C
; Patent No. 5856091
; GENERAL INFORMATION:
; APPLICANT: Brichard, Vincent; Van Pel, Aline;
; APPLICANT: Traversari, Catia; Wifel, Thomas;
; APPLICANT: Boon-Falleur, Thierry; De Plaen, Etienne
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR PROCESSED TO AT LEAST ONE TUN
; TITLE OF INVENTION: REJECTION ANTIGEN PRESENTED BY HLA-A2
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,319C
; FILING DATE: 10-JANUARY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/272,351
; FILING DATE: 8-JULY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/032,978
; FILING DATE: 18-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5856091man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5377.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 638-3884
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4129 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The sequence is preceded by an
; OTHER INFORMATION: unsequenced portion of from 4.7 to 5.3
; OTHER INFORMATION: kilobases
US-08-370-319C-12

Query Match 80.0%; Score 20; DB 2; Length 4129;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
DB 3066 GGTTCAGTGAGCCGAGATA 3085

RESULT 7

US-09-224-834-12
; Sequence 12, Application US/09224834
; Patent No. 6201111
; GENERAL INFORMATION:

APPLICANT: Brichard, Vincent; Van Pel, Aline;
APPLICANT: Traversari, Catia; W lfel, Thomas; Pierre;
APPLICANT: Boon-Falleur, Thierry; De Plaeen, Bienne
TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PERCURSOR PROCESSED TO AT LEAST ONE TU
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,834
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/370,319
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/032,978
FILING DATE: 18-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6201111man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5377.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 685-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4129 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The sequence is preceded by an
OTHER INFORMATION: unsequenced portion of from 4.7 to 5.3
OTHER INFORMATION: kilobases
US-09-224-834-12

Query Match 80.0%; Score 20; DB 3; Length 4129;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATA 20
|||||
DB 3066 GGTTCAGTGCAGCCGAGATA 3085

RESULT 8
US-08-965-048-5
Sequence 5, Application US/08965048
Patent No. 6323244
GENERAL INFORMATION:
APPLICANT: Chen, Hong
APPLICANT: Freimer, Nelson
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF NEUROPSYCHIATRIC DISORDERS
FILE REFERENCE: 7853-093
CURRENT APPLICATION NUMBER: US/08/965,048
CURRENT FILING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 45716

TYPE: DNA
ORGANISM: Homo sapiens
US-08-965-048-5

Query Match 80.0%; Score 20; DB 4; Length 45716;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATA 20
|||||
DB 33531 GGTTCAGTGCAGCCGAGATA 33550

RESULT 9
US-08-965-048-6
Sequence 6, Application US/08965048
Patent No. 6323244
GENERAL INFORMATION:
APPLICANT: Chen, Hong
APPLICANT: Freimer, Nelson
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF NEUROPSYCHIATRIC DISORDERS
FILE REFERENCE: 7853-093
CURRENT APPLICATION NUMBER: US/08/965,048
CURRENT FILING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 45989
TYPE: DNA
ORGANISM: Homo sapiens
US-08-965-048-6

Query Match 80.0%; Score 20; DB 4; Length 45989;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATA 20
|||||
DB 33645 GGTTCAGTGCAGCCGAGATA 33664

RESULT 10
US-08-133-629-2
Sequence 2, Application US/08133629
Patent No. 5597694
GENERAL INFORMATION:
APPLICANT: Munroe, David J.
APPLICANT: Housman, David E.
TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,629
FILING DATE: 07-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Greer, Helen
REGISTRATION NUMBER: 36,816
REFERENCE/DOCKET NUMBER: M0828/7001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441
TELEX: 92-1742 EZEKIEL
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-133-629-2

Query Match 76.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCCGAGAT 19
DB 3 GGTTCAGTGGCCGAGAT 21

RESULT 11
US-08-687-080-93/c
Sequence 93, Application US/08687080
Patent No. 5965427
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Denlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 5' END OF INTRON 16 OF RAD50 GENOMIC
INDIVIDUAL ISOLATE: SEQUENCE

US-08-687-080-93
Query Match 76.0%; Score 19; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCCGAGAT 19
DB 3 GGTTCAGTGGCCGAGAT 21

Db 128 GGTTCAGTGGCCGAGAT 110

RESULT 12
US-08-849-701-1
Sequence 1, Application US/08849701
Patent No. 5922544
GENERAL INFORMATION:
APPLICANT: Miyai, Kiyoshi
APPLICANT: Naitoh, Tsutomu
APPLICANT: Yonekawa, Yoshihiro
TITLE OF INVENTION: Method of Cell Detection
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,701
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/02734
FILING DATE: 27-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: EIKEN1.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Other
IMMEDIATE SOURCE:
CLONE: A1u sequence BLUR8
US-08-849-701-1

Query Match 76.0%; Score 19; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCCGAGAT 19
DB 194 GGTTCAGTGGCCGAGAT 212

RESULT 13
US-08-579-445-26
Sequence 26, Application US/08579445
Patent No. 6566053
GENERAL INFORMATION:
APPLICANT: Ferucho, Manuel
APPLICANT: Peinado, Miguel A.
APPLICANT: Ionov, Yuri
APPLICANT: Malkhosyan, Sergei
TITLE OF INVENTION: Identification of Neoplasms by Detection
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/579,445
APPLICATION NUMBER: US/08/579,445
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/152,484
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kirkpatrick, Anita M.
REGISTRATION NUMBER: 32,617
REFERENCE/DOCKET NUMBER: STRATAG.009A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-579-445-26

Query Match 76.0%; Score 19; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCCGAGAT 19
|||||
Db 218 GGTTCAGTGCAGCCGAGAT 236

RESULT 14
US-08-481-658B-61/c
Sequence 61, Application US/08/481658B
Patent No. 5955075
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-481-658B-61

Query Match 76.0%; Score 19; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCCGAGAT 19
|||||
Db 75 GGTTCAGTGCAGCCGAGAT 57

RESULT 15
US-08-477-504A-61/c
Sequence 61, Application US/08/477504A
Patent No. 5972353
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-477-504A-61

Query Match 76.0%; Score 19; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGAGCCGAGAT 19
|||
Db 75 GGTTCAGTGAGCCGAGAT 57
|||

Search completed: January 31, 2004, 17:34:49
Job time : 39.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 17:19:57 ; Search time 143 Seconds
(without alignments)
637.160 Million cell updates/sec

Title: US-09-784-423-124

Perfect score: 25

Sequence: 1 GGTTCAGTGCAGCCGAGATAGAGT 25

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2434939 seqs, 1822278265 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA.*
1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubna/US10_NEW_PUB.seq.*
17: /cgn2_6/ptodata/1/pubna/US60_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	9	US-09-784-423-124
2	25	100.0	1000	9	Sequence 124, Appl
3	21	84.0	611	13	Sequence 32, Appl
4	21	84.0	611	14	Sequence 256, Appl
5	21	84.0	619	13	Sequence 256, Appl
6	21	84.0	619	13	Sequence 256, Appl
7	21	84.0	619	13	Sequence 256, Appl
8	21	84.0	619	13	Sequence 256, Appl
9	21	84.0	619	13	Sequence 256, Appl
10	21	84.0	619	13	Sequence 256, Appl
11	21	84.0	619	13	Sequence 256, Appl
12	21	84.0	619	13	Sequence 256, Appl
13	21	84.0	619	13	Sequence 256, Appl
14	21	84.0	619	13	Sequence 256, Appl
15	21	84.0	619	13	Sequence 256, Appl
16	21	84.0	619	13	Sequence 256, Appl
17	21	84.0	619	13	Sequence 256, Appl
18	21	84.0	619	13	Sequence 256, Appl

Sequence 41283, A
Sequence 128887, A
Sequence 128887, A
Sequence 166508, A
Sequence 166508, A
Sequence 102290, A
Sequence 102290, A
Sequence 102290, A
Sequence 102290, A
Sequence 102290, A
Sequence 5690, A
Sequence 4, Appl
Sequence 7, Appl
Sequence 1, Appl
Sequence 27530, A
Sequence 138166, A
Sequence 138166, A
Sequence 2157, A
Sequence 8428, A
Sequence 148, A
Sequence 66429, A
Sequence 66429, A
Sequence 762, A
Sequence 26090, A
Sequence 91667, A
Sequence 91667, A
Sequence 91667, A
Sequence 91667, A
Sequence 291649, A
Sequence 291649, A
Sequence 281502, A

ALIGNMENTS

RESULT 1

US-09-784-423-124
; Sequence 124, Application US/09784423
; Patent No. US20020012924A1
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESS: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,423
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/018,584
; FILING DATE: 04-Feb-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 124

```

;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 25
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
;
;   SEQUENCE DESCRIPTION: SEQ ID NO: 124
US-09-784-423-124

Query Match      100.0%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 GGTTCAGTGAGCCGAGATAGAGT 25
        |||||
Db      1 GGTTCAGTGAGCCGAGATAGAGT 25

RESULT 2
US-09-784-423-32
; Sequence 32, Application US/09784423
; Patent No. US20020012924A1
; GENERAL INFORMATION:
;   APPLICANT: Schumm, James W.
;   Bacher, Jeffrey W.
;   TITLE OF INVENTION: MATERIALS AND METHODS FOR
;   IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
;   REPEAT DNA MARKERS
;
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Promega Corporation
;   STREET: 2800 Woods Hollow Road
;   CITY: Madison
;   STATE: Wisconsin
;   COUNTRY: U.S.A.
;   ZIP: 53711-5399
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
;   COMPUTER: IBM compatible PC
;   OPERATING SYSTEM: Windows 95
;   SOFTWARE: word 97 (DOS text format)
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/784,423
;   FILING DATE: 15-Feb-2001
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 09/018,584
;     FILING DATE: 04-Feb-1998
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Grady J. Frenchick
;     REGISTRATION NUMBER: 29,018
;     REFERENCE/DOCKET NUMBER: 16026.9180
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (608) 257-3501
;     TELEFAX: (608) 257-2275
;
; INFORMATION FOR SEQ ID NO: 32
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1000 bp
;     TYPE: Nucleic Acid
;     STRANDEDNESS: Double
;     TOPOLOGY: Circular
;   MOLECULE TYPE: Genomic DNA
;   HYPOTHETICAL: no
;   IMMEDIATE SOURCE:
;     CLONE: SL32
;   POSITION IN GENOME:
;     CHROMOSOME/SEGMENT: 22
;   SEQUENCE DESCRIPTION: SEQ ID NO: 32
US-09-784-423-32

Query Match      100.0%; Score 25; DB 9; Length 1000;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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SEQ ID NO 256
LENGTH: 611
TYPE: DNA
ORGANISM: Human
US-10-027-632-256

Query Match 84.0%; Score 21; DB 14; Length 611;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCCGAGATAA 21
|||
Db 343 GGTTCAGTGGCCGAGATAA 363

RESULT 5

US-10-027-632-76653/c
Sequence 76653, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 76653

LENGTH: 619
TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(619)

OTHER INFORMATION: n = A,T,C or G

US-10-027-632-76653

Query Match 84.0%; Score 21; DB 13; Length 619;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCCGAGATAA 21
|||
Db 95 GGTTCAGTGGCCGAGATAA 75

RESULT 6

US-10-027-632-76654/c
Sequence 76654, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 76654

LENGTH: 619

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(619)

OTHER INFORMATION: n = A,T,C or G

US-10-027-632-76654

Query Match 84.0%; Score 21; DB 13; Length 619;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCCGAGATAA 21
|||
Db 95 GGTTCAGTGGCCGAGATAA 75

RESULT 7

US-10-027-632-109145/c
Sequence 109145, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 109145

LENGTH: 619

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(619)

OTHER INFORMATION: n = A,T,C or G

US-10-027-632-109145

Query Match 84.0%; Score 21; DB 13; Length 619;
Best Local Similarity 100.0%; Pred. No. 0.0027;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCGAGATAA 21
 |||||
 Db 95 GGTTCAGTGCAGCGAGATAA 75

RESULT 8

US-10-027-632-109146/c
 ; Sequence 109146, Application US/10027632
 ; Publication No. US20030204075A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; POLYMORPHISMS IN THE HUMAN GENOME
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 109146
 ; LENGTH: 619
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(619)
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-027-632-109146

Query Match 84.0%; Score 21; DB 13; Length 619;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCGAGATAA 21
 |||||
 Db 95 GGTTCAGTGCAGCGAGATAA 75

RESULT 9

US-10-027-632-76653/c
 ; Sequence 76653, Application US/10027632
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; POLYMORPHISMS IN THE HUMAN GENOME
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 76653
 ; LENGTH: 619
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(619)
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-027-632-76653

Query Match 84.0%; Score 21; DB 14; Length 619;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCGAGATAA 21
 |||||
 Db 95 GGTTCAGTGCAGCGAGATAA 75

RESULT 10

US-10-027-632-76654/c
 ; Sequence 76654, Application US/10027632
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; POLYMORPHISMS IN THE HUMAN GENOME
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 76654
 ; LENGTH: 619
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(619)
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-027-632-76654

Query Match 84.0%; Score 21; DB 14; Length 619;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCGAGATAA 21
 |||||
 Db 95 GGTTCAGTGCAGCGAGATAA 75

RESULT 11

US-10-027-632-109145/c
 ; Sequence 109145, Application US/10027632

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; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109145
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(619)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-109145

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Query Match      84.0%; Score 21; DB 14; Length 619;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 GGTTCAGTGCAGCCGAGATAA 21
          |||||
Db      95 GGTTCAGTGCAGCCGAGATAA 75

```

```

RESULT 12
US-10-027-632-109146/c
; Sequence 109146, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109146
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Human
; FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: (1)..(619)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-109146

```

```

Query Match      84.0%; Score 21; DB 14; Length 619;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 GGTTCAGTGCAGCCGAGATAA 21
          |||||
Db      95 GGTTCAGTGCAGCCGAGATAA 75

```

```

RESULT 13
US-10-027-632-41282/c
; Sequence 41282, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41282
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-41282

```

```

Query Match      84.0%; Score 21; DB 13; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 GGTTCAGTGCAGCCGAGATAA 21
          |||||
Db      112 GGTTCAGTGCAGCCGAGATAA 92

```

```

RESULT 14
US-10-027-632-41283/c
; Sequence 41283, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29

```

```

; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ IDS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41293
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-41293

```

```

Query Match      84.0%; Score 21; DB 13; Length 638;
Best Local Similarity 100.0%; Pred.No. 0.0027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGTTCGAGTGAGCCGAGATAA  21
          |||
DB      112 GGTTCGAGTGAGCCGAGATAA  92

```

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RESULT 15
US-10-027-632-41282/c
/ Sequence 41282, Application US/10027632
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Polymorphisms in the
/ TITLE OF INVENTION: Polymorphisms in the
/ FILE REFERENCE: 106827.129
/ CURRENT APPLICATION NUMBER: US/10/027.632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 41282
/ LENGTH: 638
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-41282

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Query Match      84.0%; Score 21; DB 14; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGTTCAGTGAGCCGAGATAA  21
Db      112 GGTTCAGTGAGCCGAGATAA  92

```

Search completed: January 31, 2004, 17:39:48
Job time : 145 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 17:18:36 ; Search time 38.5 Seconds
(without alignments)
286.612 Million cell updates/sec

Title: US-09-784-423-125
Perfect score: 25
Sequence: 1 TGTGCGAGGACGACGAATTACAG 25

Scoring table: OLIGO.NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	3	US-09-018-584A-125
2	25	100.0	1000	3	US-09-018-584A-125
3	15	60.0	28720	4	US-09-341-587-7
4	14	56.0	627	4	US-08-981-030-2
5	14	56.0	627	4	US-08-981-030-12
6	14	56.0	682	4	US-08-981-030-1
7	14	56.0	1727	1	US-08-289-458-3
8	14	56.0	1727	2	US-08-761-549-3
9	14	56.0	1727	3	US-09-127-646-3
10	14	56.0	4376	1	US-08-119-125A-1
11	14	56.0	6744	1	US-08-119-125A-2
12	14	56.0	9493	2	US-08-639-857-23
13	14	56.0	9493	4	US-08-469-260A-163
14	14	56.0	9493	4	US-08-488-446-163
15	14	56.0	9493	4	US-08-467-344A-163
16	14	56.0	99500	4	US-09-798-096-10
17	14	56.0	1230025	4	US-09-198-452A-1
18	13	52.0	22	2	US-08-332-766A-76
19	13	52.0	56	1	US-08-229-279-6
20	13	52.0	56	1	US-08-701-269-6
21	13	52.0	89	4	US-09-511-625B-57
22	13	52.0	91	3	US-09-084-120-23
23	13	52.0	445	2	US-08-332-766A-16
24	13	52.0	558	4	US-09-252-991A-15529
25	13	52.0	611	3	US-09-328-111-416
26	13	52.0	628	4	US-09-669-751-62
27	13	52.0	646	3	US-08-998-416-77

Sequence 1545, Ap
Sequence 29, Appl
Sequence 29, Appl
Sequence 174, Appl
Sequence 174, Appl
Sequence 174, Appl
Sequence 174, Appl
Sequence 133, Appl
Sequence 133, Appl
Sequence 133, Appl
Sequence 15309, A
Sequence 26, Appl
Sequence 40, Appl
Sequence 20, Appl
Sequence 514, Appl
Sequence 515, Appl
Sequence 516, Appl
Sequence 17, Appl
Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-09-018-584A-125
Sequence 125, Application US/09018584A
Patent No. 6238863

GENERAL INFORMATION:

APPLICANT: Schumm, James W.
APPLICANT: Bacher, Jeffery W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
TITLE OF INVENTION: REPEAT DNA MARKERS
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Promega Corporation
STREET: 2800 Woods Hollow Road
CITY: Madison
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: 53711-5399

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
COMPUTER: IBM compatible PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97 (DOS text format)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,584A
FILING DATE: 04-Feb-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Grady J. Frenchick
REGISTRATION NUMBER: 29,018
REFERENCE/DOCKET NUMBER: 16026,9180
TELEPHONE: (608) 257-3501
TELEFAX: (608) 257-2275
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 25
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

US-09-018-584A-125

Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TGTGCGAGGACGACGAATTACAG 25

Db 1 TGTGCGAGGACGACGAATTACAG 25

```
RESULT 2
US-09-018-584A-32/c
; Sequence 32, Application US/09018584A
; Patent No. 6238863
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/018,584A
; FILING DATE: 04-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Circular
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: no
; IMMEDIATE SOURCE:
; CLONE: S132
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 22
US-09-018-584A-32

Query Match 100.0%; Score 25; DB 3; Length 1000;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCAAGAAATTACAG 25
Db 726 TGTGCCAGGACCAAGAAATTACAG 702

RESULT 3
US-09-341-587-7
; Sequence 7, Application US/09341587
; Patent No. 6346606
; GENERAL INFORMATION:
; APPLICANT: Mollenhauer, Jan
; TITLE OF INVENTION: Protein Containing an SRCR Domain
; FILE REFERENCE: 4121-108
; CURRENT APPLICATION NUMBER: US/09/341,587
; CURRENT FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: PCT/DE98/00096
; EARLIER FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7

Query Match 100.0%; Score 25; DB 3; Length 1000;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCAAGAAATTACAG 25
Db 726 TGTGCCAGGACCAAGAAATTACAG 702
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; LENGTH: 28720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-341-587-7

Query Match 60.0%; Score 15; DB 4; Length 28720;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGAACCAAGAAATT 20
Db 5047 CAGGAACCAAGAAATT 5061

RESULT 4
US-08-981-030-2
; Sequence 2, Application US/08981030
; Patent No. 6447783
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: FGF9 AS A SPECIFIC LIGAND FOR FGFR3
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,030
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/IL96/00011
; FILING DATE: 12-JUN-1996
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus pahari
US-08-981-030-2

Query Match 56.0%; Score 14; DB 4; Length 627;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ACCAGAAATTAC 24
Db 542 ACCAGAAATTAC 555

RESULT 5
US-08-981-030-12
; Sequence 12, Application US/08981030
; Patent No. 6447783
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: FGF9 AS A SPECIFIC LIGAND FOR FGFR3
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,030
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/IL96/00011
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; FILING DATE: 12-JUN-1996
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 627 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Rattus norvegicus
 ; US-08-981-030-12

Query Match 56.0%; Score 14; DB 4; Length 627;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ACCAGAAATTTCAC 24
 |||||
 Db 542 ACCAGAAATTTCAC 555

RESULT 6

US-08-981-030-1
 ; Sequence 1, Application US/08981030
 ; Patent No. 6447783
 ; GENERAL INFORMATION:

; APPLICANT:
 ; TITLE OF INVENTION: FGF9 AS A SPECIFIC LIGAND FOR FGFR3
 ; NUMBER OF SEQUENCES: 13
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/981,030
 ; FILING DATE:

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/IL96/00011
 ; FILING DATE: 12-JUN-1996

; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 602 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

US-08-981-030-1

Query Match 56.0%; Score 14; DB 4; Length 602;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ACCAGAAATTTCAC 24
 |||||
 Db 597 ACCAGAAATTTCAC 610

RESULT 7

US-08-289-458-3
 ; Sequence 3, Application US/08289458
 ; Patent No. 5608144
 ; GENERAL INFORMATION:

; APPLICANT: BADEN, Catherine S., DUNSMUIR, Pamela,
 ; APPLICANT: LEE, Kathleen Y.
 ; TITLE OF INVENTION: PLANT Gp2 PROMOTERS AND USES THEREOF
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: Stuart Street Tower, One Market Plaza
 ; CITY: San Francisco
 ; STATE: California

; COUNTRY: US
 ; ZIP: 94105-1493
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/289,458
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dow, Karen B.
 ; REGISTRATION NUMBER: 29,684
 ; REFERENCE/DOCKET NUMBER: 12176-4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 543-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1727 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CAAT signal
 ; LOCATION: 1100..1103
 ; FEATURE:
 ; NAME/KEY: TATA signal
 ; LOCATION: 1139..1146
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1169
 ; OTHER INFORMATION: /note= "Transcriptional start site"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1172
 ; OTHER INFORMATION: /note= "pgp50 5' end"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1234..1236
 ; OTHER INFORMATION: /note= "Translation start codon"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1298
 ; OTHER INFORMATION: /note= "Intron start site"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1..1233
 ; OTHER INFORMATION: /note= "Gp2 promoter sequence"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1..1727
 ; OTHER INFORMATION: /note= "Gp2 Genomic DNA clone"
 ; US-08-289-458-3

Query Match 56.0%; Score 14; DB 1; Length 1727;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GGAACCAAGAAATTT 21
 |||||
 Db 1619 GGAACCAAGAAATTT 1632

RESULT 8

US-08-761-549-3
 ; Sequence 3, Application US/08761549
 ; Patent No. 5981727
 ; GENERAL INFORMATION:
 ; APPLICANT: BADEN, Catherine S., DUNSMUIR, Pamela,
 ; APPLICANT: LEE, Kathleen Y.

```
;; TITLE OF INVENTION: PLANT Gp2 PROMOTERS AND USES THEREOF
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Kourile and Crew
;; STREET: Steuart Street Tower, One Market Plaza
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: US
;; ZIP: 94103-1493
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/761,549
;; FILING DATE: 06-DEC-1996
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/289,458
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Dow, Karen B.
;; REGISTRATION NUMBER: 29,684
;; REFERENCE/DOCKET NUMBER: 12176-4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 543-9600
;; TELEFAX: (415) 543-5043
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1727 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CAAT signal
;; LOCATION: 1100..1103
;; FEATURE:
;; NAME/KEY: TATA signal
;; LOCATION: 1139..1146
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1169-
;; OTHER INFORMATION: /note= "Transcriptional start site"
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1172
;; OTHER INFORMATION: /note= "pgp50 5' end"
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1234..1236
;; OTHER INFORMATION: /note= "Translation start codon"
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1298
;; OTHER INFORMATION: /note= "Intron start site"
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1..1233
;; OTHER INFORMATION: /note= "Gp2 promoter sequence"
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1..1727
;; OTHER INFORMATION: /note= "Gp2 Genomic DNA clone"
;; US-08-761-549-3
Query Match 56.0%; Score 14; DB 2; Length 1727;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GGAACCGAATTT 21
|||||
;;
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Db 1619 GGAACCGAATTT 1632

RESULT 9
US-09-127-646-3
; Sequence 3, Application US/09127646
; Patent No. 6291744
; GENERAL INFORMATION:
; APPLICANT: Baden, Catherine S.
; APPLICANT: Dunsmuir, Pamela
; APPLICANT: Lee, Kathleen Y.
; APPLICANT: DNA Plant Technology Corporation
; TITLE OF INVENTION: Nucleic Acids Encoding Plant Group 2 Proteins and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 012176-004020US
; CURRENT APPLICATION NUMBER: US/09/127,646
; CURRENT FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 08/289,458
; EARLIER FILING DATE: 1994-08-12
; EARLIER APPLICATION NUMBER: US 08/761,549
; EARLIER FILING DATE: 1996-12-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 3
; LENGTH: 1727
; TYPE: DNA
; ORGANISM: Capsicum annuum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1727)
; OTHER INFORMATION: pepper plant Group 2 (Gp2) genomic DNA clone
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1233)
; OTHER INFORMATION: Gp2 promoter sequence
; FEATURE:
; NAME/KEY: CAAT signal
; LOCATION: (1100)..(1103)
; FEATURE:
; NAME/KEY: TATA signal
; LOCATION: (1139)..(1146)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1169)
; OTHER INFORMATION: transcriptional start site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1172)
; OTHER INFORMATION: pgp50 5' end
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1234)..(1236)
; OTHER INFORMATION: translation start codon
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1298)
; OTHER INFORMATION: intron start site
; US-09-127-646-3

Query Match 56.0%; Score 14; DB 3; Length 1727;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GGAACCGAATTT 21
|||||
Db 1619 GGAACCGAATTT 1632

RESULT 10
US-08-119-125A-1
; Sequence 1, Application US/08119125A
; Patent No. 5610011
; GENERAL INFORMATION:
```

APPLICANT: SMITH, Hilda Elizabeth
APPLICANT: VECHT, Uri
TITLE OF INVENTION: DNA Sequences which code for Virulence
TITLE OF INVENTION: Characteristics of Streptococcus suis and parts thereof, polyp
TITLE OF INVENTION: antibodies derived therefrom and the use thereof for the diagn
TITLE OF INVENTION: protection against infection by S. suis in mammals, including
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Centraal Diergeneeskundig Instituut
STREET: Edelhertweg 15
CITY: PH Lelystad
STATE:
COUNTRY: The Netherlands
ZIP: NL-8219
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS v.6.0
SOFTWARE: WordPerfect v. 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,125A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL92/00054
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: NL 9100510
FILING DATE: 21-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Handal, Anthony H.
REGISTRATION NUMBER: 26275
REFERENCE/DOCKET NUMBER: SMITHHE119125
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 838-8589
TELEFAX: (203) 838-8794
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4376 base pairs
TYPE: Nucleic acid with corresponding amino acids
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Streptococcus suis type II (pathogenic)
FEATURE:
OTHER INFORMATION: Extracellular protein factor (EF) gene
NAME/KEY: promoter -35 region
LOCATION: bp 66 to 71
FEATURE:
NAME/KEY: promoter -10 region
LOCATION: bp 89 to 94
FEATURE:
NAME/KEY: promoter -35 region
LOCATION: bp 153 to 158
FEATURE:
NAME/KEY: promoter -10 region
LOCATION: bp 176 to 181
FEATURE:
NAME/KEY: ribosome binding site
LOCATION: bp 350 to 356
FEATURE:
NAME/KEY: signal peptide
LOCATION: bp 361 to 498
FEATURE:
NAME/KEY: mature peptide
LOCATION: bp 499 to 2890
FEATURE:
NAME/KEY: dyad symmetry regions
LOCATION: from bp 4186 to 4198 and from bp 4203 to 4215
FEATURE:
NAME/KEY: dyad symmetry regions
LOCATION: from bp 4243 to 4257 and from bp 4263 to 4276

US-08-119-125A-1

Query Match 56.0%; Score 14; DB 1; Length 4376;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGAACCAAGAAAT 19

DB 314 CAGGAACCAAGAAAT 327

RESULT 11

US-08-119-125A-2

; Sequence 2, Application US/08119125A

; Patent No. 5610011

; GENERAL INFORMATION:

; APPLICANT: SMITH, Hilda Elizabeth

; APPLICANT: VECHT, Uri

; TITLE OF INVENTION: DNA Sequences which code for Virulence

; TITLE OF INVENTION: Characteristics of Streptococcus suis and parts thereof, polyp

; TITLE OF INVENTION: antibodies derived therefrom and the use thereof for the diagn

; TITLE OF INVENTION: protection against infection by S. suis in mammals, including ;

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Centraal Diergeneeskundig Instituut

; STREET: Edelhertweg 15

; CITY: PH Lelystad

; STATE:

; COUNTRY: The Netherlands

; ZIP: NL-8219

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS-DOS v.6.0

; SOFTWARE: WordPerfect v. 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/119,125A

; FILING DATE: 20-SEP-1993

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/NL92/00054

; FILING DATE: 19-MAR-1992

; APPLICATION NUMBER: NL 9100510

; FILING DATE: 21-MAR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Handal, Anthony H.

; REGISTRATION NUMBER: 26275

; REFERENCE/DOCKET NUMBER: SMITHHE119125

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (203) 838-8589

; TELEFAX: (203) 838-8794

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6744 base pairs

; TYPE: Nucleic acid with corresponding amino acids

; STRANDEDNESS: single stranded

; TOPOLOGY: linear

; MOLECULE TYPE: genomic DNA

; ORIGINAL SOURCE:

; ORGANISM: Streptococcus suis type II (pathogenic)

; FEATURE:

; OTHER INFORMATION: Extracellular factor related protein (EF*) gene

; FEATURE:

; NAME/KEY: promoter -35 region

; LOCATION: bp 66 to 71

; FEATURE:

; NAME/KEY: promoter -10 region

; LOCATION: bp 89 to 94

; FEATURE:

; NAME/KEY: promoter -35 region

; LOCATION: bp 153 to 158

; FEATURE:

; NAME/KEY: promoter -10 region

; LOCATION: bp 153 to 158

; NAME/KEY: promoter -10 region

; LOCATION: bp 153 to 158


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; LOCATION: bp 176 to 181
; FEATURE:
; NAME/KEY: ribosome binding site
; LOCATION: bp 350 to 356
; FEATURE:
; NAME/KEY: signal peptide
; LOCATION: bp 361 to 438
; FEATURE:
; NAME/KEY: start of repetitive units RI-R11
; LOCATION: bp 2869, 3097, 3292, 3520, 4087, 4381, 4609, 4837,
; LOCATION: 5065, 5293, 5521;
; FEATURE:
; NAME/KEY: start of repetitive Asn-Pro-Asn-Ieu sequences
; LOCATION: bp 2932, 3160, 3355, 3583, 4150, 4444, 4672, 4900,
; LOCATION: 5128, 5356, 5584;
; FEATURE:
; NAME/KEY: dyad symmetry regions
; LOCATION: from bp 6554 to 6566 and from bp 6571 to 6583
; FEATURE:
; NAME/KEY: dyad symmetry regions
; LOCATION: from bp 6611 to 6625 and from bp 6631 to 6644
; US-08-119-125A-2
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; Query Match 56.0%; Score 14; DB 1; Length 6744;
; Best Local Similarity 100.0%; Pred. No. 28;
; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 6 CAGGAACCAAGAAAT 19
DB 314 CAGGAACCAAGAAAT 327
;
RESULT 12
US-08-639-857-23
; Sequence 23, Application US/08639857
; Patent No. 5955318
; GENERAL INFORMATION:
; APPLICANT: Simons, J. N.
; APPLICANT: Desai, S. M.
; APPLICANT: Mushahwar, I. K.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR CONTROLLING THE
; TITLE OF INVENTION: TRANSLATION OF HEPATITIS GB PROTEINS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Rd
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/639,857
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5793.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-0378
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9493 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
; Query Match 56.0%; Score 14; DB 1; Length 6744;
; Best Local Similarity 100.0%; Pred. No. 28;
; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 6 CAGGAACCAAGAAAT 19
DB 314 CAGGAACCAAGAAAT 327
;
RESULT 13
US-08-469-260A-163
; Sequence 163, Application US/08469260A
; Patent No. 6451378
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BULJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9493 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-469-260A-163
;
; Query Match 56.0%; Score 14; DB 4; Length 9493;
; Best Local Similarity 100.0%; Pred. No. 29;
; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 TGTGCCAGGAACCA 14
DB 4037 TGTGCCAGGAACCA 4050
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US-08-639-857-23
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; Query Match 56.0%; Score 14; DB 2; Length 9493;
; Best Local Similarity 100.0%; Pred. No. 29;
; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 TGTGCCAGGAACCA 14
DB 4037 TGTGCCAGGAACCA 4050
;
RESULT 13
US-08-469-260A-163
; Sequence 163, Application US/08469260A
; Patent No. 6451378
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BULJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9493 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-469-260A-163
;
; Query Match 56.0%; Score 14; DB 4; Length 9493;
; Best Local Similarity 100.0%; Pred. No. 29;
; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 TGTGCCAGGAACCA 14
DB 4037 TGTGCCAGGAACCA 4050
;

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RESULT 14

US-08-488-446-163
; Sequence 163, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9493 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-488-446-163

Query Match 56.0%; Score 14; DB 4; Length 9493;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACCA 14

Db 4037 TGTGCCAGGAACCA 4050

RESULT 15

US-08-467-344A-163
; Sequence 163, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY

ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,344A
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,550
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: POREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 163:
SEQUENCE CHARACTERISTICS:
LENGTH: 9493 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 163:
US-08-467-344A-163

Query Match 56.0%; Score 14; DB 4; Length 9493;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACCA 14

Db 4037 TGTGCCAGGAACCA 4050

Search completed: January 31, 2004, 17:34:51
Job time : 40.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 17:19:57 ; Search time 143 Seconds
(without alignments)
637.160 Million cell updates/sec

Title: US-09-784-423-125

Perfect score: 25

Sequence: 1 TGTCCGAGACAGAAATTTACAG 25

Scoring table:

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Gapop 60.0 , Gapext 60.0

Searched: 2434939 seqs, 1822278265 residues

Word size : 0

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : Published Applications NA.*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	US-09-784-423-125	Sequence 125, App
2	25	100.0	1000	US-09-784-423-32	Sequence 32, Appl
3	17	68.0	624	US-10-027-632-311837	Sequence 311837,
4	17	68.0	624	US-10-027-632-311837	Sequence 311837,
5	17	68.0	7273	US-10-017-161-1629	Sequence 1629, Ap
6	16	64.0	442	US-09-864-761-11479	Sequence 11479, A
7	16	64.0	494	US-10-027-632-179918	Sequence 179918,
8	16	64.0	494	US-10-027-632-179918	Sequence 179918,
9	16	64.0	624	US-10-027-632-220234	Sequence 220234,
10	16	64.0	624	US-10-027-632-220235	Sequence 220235,
11	16	64.0	624	US-10-027-632-220234	Sequence 220234,
12	16	64.0	624	US-10-027-632-220235	Sequence 220235,
13	16	64.0	641	US-10-027-632-114443	Sequence 114443,
14	16	64.0	641	US-10-027-632-114443	Sequence 114443,
15	16	64.0	1630	US-10-027-632-253734	Sequence 253734,

c	16	64.0	1630	14	US-10-027-632-253734	Sequence 253734,
	17	64.0	1791	13	US-09-814-353-21503	Sequence 21503, A
	18	60.0	315	12	US-10-242-535A-25180	Sequence 25180, A
	19	60.0	538	13	US-10-027-632-81341	Sequence 81341, A
	20	60.0	538	13	US-10-027-632-82646	Sequence 82646, A
	21	60.0	538	13	US-10-027-632-180681	Sequence 180681,
	22	60.0	538	13	US-10-027-632-301780	Sequence 301780,
	23	60.0	538	14	US-10-027-632-81341	Sequence 81341, A
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	25	60.0	538	14	US-10-027-632-180681	Sequence 180681,
	26	60.0	538	14	US-10-027-632-301780	Sequence 301780,
	27	60.0	548	13	US-10-027-632-66186	Sequence 66186, A
	28	60.0	548	13	US-10-027-632-299033	Sequence 299033,
	29	60.0	548	14	US-10-027-632-66186	Sequence 66186, A
	30	60.0	548	14	US-10-027-632-299033	Sequence 299033,
	31	60.0	569	10	US-09-917-800A-198	Sequence 198, App
	32	60.0	569	12	US-10-388-334-331	Sequence 331, App
	33	60.0	582	13	US-10-029-386-1285	Sequence 1285, Ap
	34	60.0	598	13	US-10-027-632-232023	Sequence 232023,
	35	60.0	598	14	US-10-027-632-232023	Sequence 232023,
	36	60.0	621	13	US-10-027-632-258272	Sequence 258272,
	37	60.0	621	14	US-10-027-632-258272	Sequence 258272,
	38	60.0	629	13	US-10-027-632-236107	Sequence 236107,
	39	60.0	629	14	US-10-027-632-236107	Sequence 236107,
	40	60.0	653	13	US-10-027-632-23519	Sequence 23519, A
	41	60.0	653	13	US-10-027-632-23519	Sequence 23519, A
	42	60.0	653	13	US-10-027-632-23521	Sequence 23521, A
	43	60.0	653	13	US-10-027-632-23522	Sequence 23522, A
	44	60.0	653	14	US-10-027-632-23519	Sequence 23519, A
	45	60.0	653	14	US-10-027-632-23519	Sequence 23519, A

ALIGNMENTS

RESULT 1

US-09-784-423-125
; Sequence 125, Application US/09784423
; Patent No. US20020012924A1

GENERAL INFORMATION:

APPLICANT: Schumm, James W.

ACHAR, Jeffrey W.

TITLE OF INVENTION: MATERIALS AND METHODS FOR

IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM

REPEAT DNA MARKERS

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Promega Corporation

STREET: 2800 Woods Hollow Road

CITY: Madison

STATE: Wisconsin

COUNTRY: U.S.A.

ZIP: 53711-5399

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb

COMPUTER: IBM compatible PC

OPERATING SYSTEM: Windows 95

SOFTWARE: Word 97 (DOS text format)

CURRENT APPLICATION DATA: US/09/784,423

FILING DATE: 15-Feb-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/018,584

FILING DATE: 04-Feb-1998

ATTORNEY/AGENT INFORMATION:

NAME: Grady J. Frenchick

REGISTRATION NUMBER: 29,018

REFERENCE/DOCKET NUMBER: 16026.9180

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 257-3501

TELEFAX: (608) 257-2275

INFORMATION FOR SEQ ID NO: 125

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 25
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 125
US-09-784-423-125

Query Match      100.0%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCAAGAAATTACAG 25
DB 1 TGTGCCAGGACCAAGAAATTACAG 25

RESULT 2
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; Sequence 32, Application US/09784423
; Patent No. US20020012924A1
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,423
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/018,584
; FILING DATE: 04-Feb-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 32
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1000 bp
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Double
;   TOPOLOGY: Circular
;   MOLECULE TYPE: Genomic DNA
;   HYPOTHETICAL: no
;   IMMEDIATE SOURCE:
;   CLONE: S132
;   POSITION IN GENOME:
;   CHROMOSOME/SEGMENT: 22
; SEQUENCE DESCRIPTION: SEQ ID NO: 32
US-09-784-423-32

Query Match      100.0%; Score 25; DB 9; Length 1000;
Best Local Similarity 100.0%; Pred. No. 9.7e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TGTGCCAGGACCAAGAAATTACAG 25
DB 726 TGTGCCAGGACCAAGAAATTACAG 702

RESULT 3
US-10-027-632-311837/c
; Sequence 311837, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 311837
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-311837

Query Match      68.0%; Score 17; DB 13; Length 624;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGAACCAAGAAATTTA 22
DB 536 CAGGAACCAAGAAATTTA 520

RESULT 4
US-10-027-632-311837/c
; Sequence 311837, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0

```

; SEQ ID NO 311837
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-311837

Query Match 68.0%; Score 17; DB 14; Length 624;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGACCAAGAAATTTA 22
Db 536 CAGGACCAAGAAATTTA 520

RESULT 5
US-10-017-161-1629/c
; Sequence 1629, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1629
; LENGTH: 7273
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(7273)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(264)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1125)..(1354)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1572)..(1721)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1955)..(2086)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3141)..(3257)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4706)..(4858)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5577)..(5698)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5963)..(6231)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6857)..(6926)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6998)..(7073)
US-10-017-161-1629

Query Match 68.0%; Score 17; DB 13; Length 7273;
Best Local Similarity 100.0%; Pred. No. 4.4;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 TGCCAGGACCAAGAAAT 19
Db 3978 TGCCAGGACCAAGAAAT 3962

RESULT 6
US-09-864-761-11479/c
; Sequence 11479, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 11479
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005961.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
US-09-864-761-11479

Query Match 64.0%; Score 16; DB 9; Length 442;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACACAGA 16
|||||
DB 226 TGTGCCAGGAACACAGA 211

RESULT 7

US-10-027-632-179918/c
; Sequence 179918, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179918
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-179918

Query Match 64.0%; Score 16; DB 13; Length 494;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACACAGA 16
|||||
DB 49 TGTGCCAGGAACACAGA 34

RESULT 8

US-10-027-632-179918/c
; Sequence 179918, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179918
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-179918

Query Match 64.0%; Score 16; DB 14; Length 494;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACACAGA 16
|||||
DB 49 TGTGCCAGGAACACAGA 34

RESULT 9

US-10-027-632-220234/c
; Sequence 220234, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220234
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220234

Query Match 64.0%; Score 16; DB 13; Length 624;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACAGAAATTTA 22
|||||
DB 357 AGGAACAGAAATTTA 342

RESULT 10

US-10-027-632-220235/c
; Sequence 220235, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006

```
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220235
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220235
```

```
Query Match          64.0%; Score 16; DB 13; Length 624;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 AGGAACCGAAGATTTA 22
        |||||
Db      357 AGGAACCGAAGATTTA 342
```

```
RESULT 11
US-10-027-632-220234/c
; Sequence 220234, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220234
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220234
```

```
Query Match          64.0%; Score 16; DB 14; Length 624;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 AGGAACCGAAGATTTA 22
        |||||
Db      357 AGGAACCGAAGATTTA 342
```

```
RESULT 12
US-10-027-632-220235/c
```

```
; Sequence 220235, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220235
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220235
```

```
Query Match          64.0%; Score 16; DB 14; Length 624;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 AGGAACCGAAGATTTA 22
        |||||
Db      357 AGGAACCGAAGATTTA 342
```

```
RESULT 13
US-10-027-632-114443
; Sequence 114443, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114443
; LENGTH: 641
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114443
```

```
Query Match          64.0%; Score 16; DB 13; Length 641;
```

Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCCAGGAGCAGCA 16
Db 227 TGTCCAGGAGCAGCA 242

RESULT 14
US-10-027-632-114443
; Sequence 114443, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114443
; LENGTH: 641
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-114443

Query Match 64.0%; Score 16; DB 14; Length 641;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCCAGGAGCAGCA 16
Db 227 TGTCCAGGAGCAGCA 242

RESULT 15
US-10-027-632-253734/c
; Sequence 253734, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253734
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-253734

Query Match 64.0%; Score 16; DB 13; Length 1630;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCAGGAGCAGCAAAATT 20
Db 898 CCAGGAGCAGCAAAATT 883

Search completed: January 31, 2004, 17:39:49
Job time : 144 secs